

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 27, 2004, 13:11:24 ; Search time 16 Seconds
(without alignments)
1052.371 Million cell updates/sec

Title: 10032108-2EDIT
Perfect score: 901
Sequence: 1 MTPLGPASSLPOSFLRLCLE.....SHLQSFLEVSRYVLRHLAQP 175
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	887	98.4	204	1 FQHUGL	granulocyte colony
2	875.5	97.2	207	2 A24573	granulocyte colony
3	741	82.2	194	2 T09255	granulocyte colony
4	735	81.6	174	2 T10268	granulocyte colony
5	636	70.6	208	2 A26496	granulocyte colony
6	629	69.8	214	2 JC5043	granulocyte colony
7	301	33.4	201	2 A42247	myelomonocytic gro
8	103.5	11.5	212	2 I46590	interleukin 6 - pi
9	103.5	11.5	212	2 I46521	prointerleukin 6
10	95	10.5	208	2 T09216	interleukin-6 prec
11	94	10.4	345	2 C82270	hypothetical prote
12	89	9.9	502	2 S46506	H+-transporting tw
13	88.5	9.8	666	2 A87577	oligopeptide trans
14	86.5	9.6	2175	1 S03170	homeotic protein c
15	85.5	9.5	786	2 F83292	probable sensor/re
16	84	9.3	208	1 A56610	interleukin-6 prec
17	83.5	9.3	207	2 I46084	interleukin 6 - ca
18	81	9.0	274	1 C69362	conserved hypothet
19	80.5	8.9	406	2 B72766	probable threonyl-
20	80.5	8.9	846	2 JC7721	aryl hydrocarbon r
21	80	8.9	474	2 D75550	probable D-alanyl-
22	79.5	8.8	316	2 H82958	homoserine kinase
23	79.5	8.8	325	2 T41921	hypothetical prote
24	79	8.8	423	2 AC3553	4-aminobutyrate tr
25	79	8.8	469	2 AD1926	hypothetical prote
26	77.5	8.6	254	2 S34724	probable oxidoredu
27	77.5	8.6	506	2 T07942	probable squalene
28	77.5	8.6	653	2 C82580	oligopeptide trans
29	76.5	8.5	195	2 JH0680	ciliary neurotroph

ALIGNMENTS

RESULT 1

FQHUGL

granulocyte colony-stimulating factor precursor - human

N;Alternate names: colony-stimulating factor 3; G-CSF

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1988 #sequence revision 18-Aug-1995 #text_change 09-Jul-2004

C;Accession: A25093; A49796; A47587; S68331

R;Nagata, S.; Tsuchiya, M.; Asano, S.; Yamamoto, O.; Hirata, Y.; Kubota, N.; Oheda, M.;

EMBO J. 5, 575-581, 1986

A;Title: The chromosomal gene structure and two mRNAs for human granulocyte colony-stimul

A;Reference number: A25093; MUID:86220137; PMID:2423327

A;Accession: A25093

A;Molecule type: DNA: mRNA

A;Residues: 1-204 <NAG>

A;Cross-references: UNIPROT:P09919; EMBL:X03656; EMBL:X03655; NID:g31693; PIDN:CAA27290.1

R;Devlin, J.J.; Devlin, P.E.; Myambo, K.; Lilly, M.B.; Rado, T.A.; Warren, M.K.

J. Leukoc. Biol. 41, 302-306, 1987

A;Title: Expression of granulocyte colony-stimulating factor by human cell lines.

A;Reference number: A49796; MUID:87196936; PMID:3494801

A;Accession: A49796

A;Molecule type: mRNA

A;Residues: 1-204 <DEV>

A;Cross-references: GB:M17706; NID:g183040; PIDN:AAA35882.1; PID:g183041

R;Souza, L.M.; Boons, T.C.; Gabrilove, J.; Lai, P.H.; Zsebo, K.M.; Murdock, D.C.; Chazin,

Science 232, 61-65, 1986

A;Title: Recombinant human granulocyte colony-stimulating factor: effects on normal and

A;Reference number: A47587; MUID:86151684; PMID:2420009

A;Accession: A47587

A;Molecule type: mRNA

A;Residues: 19-204 <SOU>

A;Cross-references: GB:M13008; NID:g183044; PIDN:AAA03056.1; PID:g183045

R;Hant, M.; Horan, T.; Arakawa, T.; Le, J.; Katta, V.; Rohde, M.F.

Arch. Biochem. Biophys. 324, 344-356, 1995

A;Title: Extracellular domain of granulocyte-colony stimulating factor receptor.

A;Reference number: S68331; MUID:96132662; PMID:8554326

A;Accession: S68331

A;Molecule type: protein

A;Residues: 1-131 <HAN>

C;Genetics:

A;Gene: GDB:CSF3

A;Cross-references: GDB:119083; OMIM:138970

A;Map position: 17q11.2-17q12

A;Introns: 14/1; 65/3; 101/3; 150/3

C;Function:

A;Description: stimulates the differentiation and proliferation of hematopoietic progenit

C;Superfamily: Interleukin-6

C;Keywords: cytokine; glycoprotein; growth factor; macrophage; monomer

F;1-30/Domain: signal sequence #status predicted <SIG>

F;31-204/Product: granulocyte colony-stimulating factor #status predicted <MAT>

F;66-72,94-104/Disulfide bonds: #status predicted

R;Tsuchiya, M.; Kaziro, Y.; Nagata, S.
Eur. J. Biochem. 165, 7-12, 1987
A;Title: The chromosomal gene structure for murine granulocyte colony-stimulating factor
A;Reference number: A29536; MUID:87190474; PMID:3494605
A;Accession: A29536
A;Molecule type: DNA
A;Residues: 1-208 <TSU>
A;Cross-references: UNIPROT:P09920; GB:X05402; NID:G51059; PIDN:CAA28986.1; PID:G51060
R;Tsuchiya, M.; Asano, S.; Kaziro, Y.; Nagata, S.
Proc. Natl. Acad. Sci. U.S.A. 83, 7633-7637, 1986
A;Title: Isolation and characterization of the cDNA for murine granulocyte colony-stimulating factor
A;Reference number: A26496; MUID:87017003; PMID:3489940
A;Accession: A26496
A;Molecule type: mRNA
A;Residues: 1-208 <TS>
A;Cross-references: UNIPROT:P09920; GB:X05402; NID:G51059; PIDN:CAA28986.1; PID:G51060
R;Simpson, R.J.; Nice, E.C.; Nicola, N.A.
Biol. Chem. Hoppe-Seyler 368, 1327-1331, 1987
A;Title: Structural studies on the murine granulocyte colony-stimulating factor.
A;Reference number: S02493; MUID:88106998; PMID:3501294
A;Accession: S02493
A;Status: preliminary
A;Molecule type: protein
A;Residues: 31-34, 'X', 36-43; 48-51, 'X', 53-57; 'X', 60-71; 159-164, 'X', 166-176; 183-198, 'X', 200-201
C;Genetics:
A;Introns: 14/1; 71/3; 107/3; 156/3
C;Superfamily: Interleukin-6
C;Keywords: cytokine; growth factor; macrophage; monomer
Query Match 70.6%; Score 636; DB 2; Length 208;
Best Local Similarity 73.4%; Pred. No. 3.66-53;
Matches 127; Conservative 13; Mismatches 33; Indels 0; Gaps 0;
QY 1 MTPGLPASSLPQSFLLRCLEQVRKIQDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
DB 36 VSLPPLPSLPFRSLKSLSEQVRKIQASGVLEQLCATYKLCHEPELVLLGHSIGIPKA 95
QY 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELGTPLDTLQLDVADPATTIWO 120
DB 96 SLSCSSQALQOQTKCLSQLHSGFLYQGLLQALSGISPALAPTDLQLDVANFATTIWO 155
QY 121 QMEELGMAPALQTOGAMPAPASAFORRAGGVLVASHLQSFLEVSRYVLRHLA 173
DB 156 QMENLGVAFTVQTSAMPAPASAFORRAGGVLVASHLQSFLEVSRYVLRHLA 208
RESULT 6
JC5043
granulocyte colony-stimulating factor precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Jan-1997 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
C;Accession: JC5043
R;Han, S.W.; Ramesh, N.; Osborne, W.R.A.
Gene 175, 101-104, 1996
A;Title: Cloning and expression of the cDNA encoding rat granulocyte colony-stimulating factor
A;Reference number: JC5043; MUID:97074656; PMID:8917083
A;Accession: JC5043
A;Molecule type: mRNA
A;Residues: 1-214 <HAN>
A;Cross-references: UNIPROT:P97712; GB:U37101; NID:G1680658; PIDN:AACS2915.1; PID:G16806
A;Experimental source: skin fibroblasts
C;Comment: This receptor acts on precursor hemopoietic cells to control the production of interleukin-6
C;Superfamily: Interleukin-6
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-214/Product: granulocyte colony-stimulating factor #status predicted <MAT>
Query Match 69.8%; Score 629; DB 2; Length 214;
Best Local Similarity 71.4%; Pred. No. 1.7e-52;
Matches 125; Conservative 14; Mismatches 36; Indels 0; Gaps 0;
QY 1 MTPGLPASSLPQSFLLRCLEQVRKIQDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
DB 27 VSSLPPLPSLPFRSLKSLSEQVRKIQARNTLEQLCATYKLCHEPELVLLGHSIGIPKA 86

QY 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELGTPLDTLQLDVADPATTIWO 120
DB 87 SLSCSSQALQOQTKCLSQLHSGFLYQGLLQALSGISPALAPTDLQLDVANFATTIWO 146
QY 121 QMEELGMAPALQTOGAMPAPASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 147 QMESLGVAFTVQTSAMPAPASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 201
RESULT 7
A42247
myelomonocytic growth factor precursor - chicken
N;Alternate names: colony-stimulating factor CMGF
C;Species: Gallus gallus (chicken)
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A42247; S03633
R;Sternneck, E.; Blattner, C.; Graf, T.; Leutz, A.
Mol. Cell. Biol. 12, 1728-1735, 1992
A;Title: Structure of the chicken myelomonocytic growth factor gene and specific activation of the gene
A;Reference number: A42247; MUID:92195319; PMID:1549124
A;Accession: A42247
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-201 <STE>
A;Cross-references: UNIPROT:P13854
A;Note: sequence extracted from NCBI backbone (NCBI:89832, NCBIP:89836)
R;Leutz, A.; Damm, K.; Sternneck, E.; Kowenz, E.; Frank, R.; Gausepohl, H.; Pan, E.M.O. J. 8, 175-181, 1989
A;Title: Molecular cloning of the chicken myelomonocytic growth factor (CMGF) reveals relationship to interleukin-6
A;Reference number: S03633; MUID:89231616; PMID:2785450
A;Accession: S03633
A;Molecule type: mRNA
A;Residues: 1-201 <LEU>
A;Cross-references: EMBL:X14477; NID:G63596; PIDN:CAA32639.1; PID:G63597
C;Superfamily: Interleukin-6
C;Keywords: glycoprotein

Query Match 33.4%; Score 301; DB 2; Length 201;
Best Local Similarity 40.0%; Pred. No. 2.7e-21;
Matches 66; Conservative 29; Mismatches 68; Indels 2; Gaps 1;
QY 12 QSFLLRCLEQVRKIQDGAALQERLCATYRLCHPELVLLGHSIGIPWAPLSSCPQALQ 71
DB 36 QLFLLKXNLEFTTKIRGDVAALQAVCDTFLCTEELQLVQDPDPLVQAPLDOCHKRGFQ 95
QY 72 LAGCLSQLHSGFLYQGLLQALEGISPELGTPLDTLQLDVADPATTIWOQMEELGMAPAL 131
DB 96 AEVCFQIRAGLHAYHDSLGAVLRLLPNHTTLVETLQDLAANLSSNIQQQMEDGLDITVT 155
QY 132 QPTQ--GAMPAPASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQ 174
DB 156 LPAEQRSPPTFTSGPPQQVGGFFILANQRFLETAYRALRLAR 200

RESULT 8
I46590
interleukin 6 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C;Accession: I46590
R;Mathialagan, N.; Bixby, J.; Roberts, M.R.
Mol. Reprod. Dev. 32, 324-330, 1992
A;Title: Expression of interleukin-6 in porcine, ovine, and bovine preimplantation conceptuses
A;Reference number: I46590; MUID:92360284; PMID:1497880
A;Accession: I46590
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-212 <MAT>
A;Cross-references: UNIPROT:P26893; GB:M80258; NID:G164514; PIDN:AAC27127.1; PID:G164515

C;Genetics:

A;Gene: IL-6

C;Superfamily: interleukin-6

Query Match 11.5%; Score 103.5; DB 2; Length 212;
Best Local Similarity 22.4%; Pred. No. 0.018;
Matches 35; Conservative 31; Mismatches 85; Indels 5; Gaps 3;

QY 20 EQVRKIQDGAALQERLCATYRLCHPEELVLLGHSIGIP-WAPLSSCPQALQAGCLSQ 78
DB 55 ELIKYILGKISARKKCKEYKCKENSKEVLAENNLNLPKMAEKDGCFOGFGNQETCLMR 114
QY 79 LHSGFLYQGLLQALEGISPELGTPLDTLQDVADEATTIQQMEELGMAPALQPT--QG 136
DB 115 ITTGLVEFQIYLDYLOKEYESNKGNEAVQISTKALIQTLRQKGNPKATTPNPTNAG 174
QY 137 AMPAFAS--AFQRRAGGVLVASHLQSFLEVSRYVLR 170
DB 175 LLDKLSQNEWMKNTKIILIRSLSDFLQFSRAIR 210

RESULT 9

I46621

prointerleukin 6 - pig

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004

C;Accession: I46621

R;Richards, C.; Saklatva, J.

Cytokine 3, 269-276, 1991

A;Title: Molecular Cloning and Sequence of Porcine Interleukin 6 cDNA and Expression of

A;Reference number: I46621; MUID:91338547; PMID:1873476

A;Accession: I46621

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-212 <RCL>

A;Cross-references: UNIPROT:P26893; GB:M86722; NID:g164624; PIDN:AAC3733.1; PID:g164625

C;Genetics:

A;Gene: IL6

C;Superfamily: interleukin-6

Query Match 11.5%; Score 103.5; DB 2; Length 212;
Best Local Similarity 22.4%; Pred. No. 0.018;
Matches 35; Conservative 31; Mismatches 85; Indels 5; Gaps 3;

QY 20 EQVRKIQDGAALQERLCATYRLCHPEELVLLGHSIGIP-WAPLSSCPQALQAGCLSQ 78
DB 55 ELIKYILGKISARKKCKEYKCKENSKEVLAENNLNLPKMAEKDGCFOGFGNQETCLMR 114
QY 79 LHSGFLYQGLLQALEGISPELGTPLDTLQDVADEATTIQQMEELGMAPALQPT--QG 136
DB 115 ITTGLVEFQIYLDYLOKEYESNKGNEAVQISTKALIQTLRQKGNPKATTPNPTNAG 174
QY 137 AMPAFAS--AFQRRAGGVLVASHLQSFLEVSRYVLR 170
DB 175 LLDKLSQNEWMKNTKIILIRSLSDFLQFSRAIR 210

RESULT 10

T09216

interleukin-6 precursor - horse

C;Species: Equus caballus (domestic horse)

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C;Accession: T09216

R;Sviderski, C.E.; Horohov, D.W.

submitted to the EMBL Data Library, July 1996

A;Reference number: Z16613

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-208 <SWI>

A;Cross-references: UNIPROT:Q95181; EMBL:U64794; NID:g2654387; PID:g2654388

C;Genetics:

A;Gene: IL-6

C;Superfamily: interleukin-6

C;Keywords: cytokine; growth factor

Query Match 10.5%; Score 95; DB 2; Length 208;
Best Local Similarity 21.0%; Pred. No. 0.12;
Matches 37; Conservative 35; Mismatches 96; Indels 8; Gaps 3;

QY 3 PLGRASSLPQSFL---RCLEQVRKIQDGAALQERLCATYRLCHPEELVLLGHSIGIP 58
DB 31 PLGEDTTTNGSLTTADTKTQHIKVIYLGKISARKKCKENNFCKENSKENSVLAENNLNLP 90
QY 59 WAPLSSCPQALQAGCLSQHSGFLYQGLLQALEGISPELGTPLDTLQDVADEATT 117
DB 91 KMAEKDGCFOGFGNQETCLMKITTTGLSEFQIYVLEYLQNEFKGEKENITQWISTKVLVQI 150
QY 118 IWQOMEELGMA---PALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLR 170
DB 151 LMQKMKNEVTPDPTAKSSLLAKLHNSQNEWMKNTTTHILRSLEDFLQFSRAVR 206

RESULT 11

C82270

hypothetical protein VC0886 [imported] - Vibrio cholerae (strain N16961 serogroup O1)

C;Species: Vibrio cholerae

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C;Accession: C82270

R;Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-345 <HEI>

A;Cross-references: UNIPROT:Q9KTL6; GB:AE004172; GB:AE003852; NID:g9655323; PIDN:AAF94041

A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics:

A;Gene: VC0886

A;Map position: 1

Query Match 10.4%; Score 94; DB 2; Length 345;
Best Local Similarity 32.2%; Pred. No. 0.27;
Matches 38; Conservative 15; Mismatches 43; Indels 22; Gaps 6;

QY 8 SSILPQSFLRLCLEQVRKIQDGAALQERLC-----ATYRLCHPEELVLLGHSIGIPWAPLS 63
DB 228 ASDPDLFLLAAL--VRALAGAPANILDATCDAILASPAICHPEVLIALA---GRSWSLE 282
QY 64 S---CPSQALQAGCLSQ-LHSGFLYQGLLQALEGI-----SPELGTPLDTLQ 108
DB 283 NSGRAQRFLIRLAQTQNLQFNQFADVVVLPALRGVMLPLLHASPSPLELALEQLQ 340

RESULT 12

S46506

H+-transporting two-sector ATPase (EC 3.6.3.14) protein 6 - beet mitochondrion

N;Alternate names: F0-ATPase chain 6

C;Species: mitochondrion Beta vulgaris (beet)

C;Date: 15-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004

C;Accession: S46506; S46505; S21339

R;Xue, Y.; Collin, S.; Davies, D.R.; Thomas, C.M.

Plant Mol. Biol. 25, 91-103, 1994

A;Title: Differential screening of mitochondrial cDNA libraries from male-fertile and cy

A;Reference number: S46505; MUID:94272017; PMID:8003700

A;Accession: S46506

A;Molecule type: DNA

A;Residues: 1-502 <XUE>

A;Cross-references: UNIPROT:Q34008; EMBL:X54722; NID:g510146; PIDN:CAA38524.1; PID:g5101

A;Experimental source: male-sterile CMS

A;Note: in the authors' translation residues 75-86 do not match the nucleotide sequence

A;Note: the authors translated the codon ATG for residue 442 as Phe

A;Accession: S03170
A;Molecule type: mRNA
A;Residues: 1-2175 <BLO>
A/Cross-references: UNIPROT:P10180; EMBL:X07985; NID:g7767; PIDN:CAA30794.1; PID:g7768
C;Genetics:
A;Gene: cut
A/Cross-references: FlyBase:FBgn0004198
C/Superfamily: homeotic protein cut; cut repeat homology; homeobox homology
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation
F/886-958/Domain: cut repeat homology <CU1>
F/1339-1411/Domain: cut repeat homology <CU2>
F/1617-1689/Domain: cut repeat homology <CU3>
F/1746-1802/Domain: homeobox homology <HOX>

Query Match 9.6%; Score 86.5; DB 1; Length 2175;
Best Local Similarity 23.1%; Pred. No. 13;
Matches 34; Conservative 21; Mismatches 61; Indels 31; Gaps 3;

Qy 28 DGAMQLRCLCATYRLCHPEELVLLGHSIGIPWAPLSGPCSQALQLAGCLSGLHSGFLFYQ 87
Db | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
 | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1404 DENAVHKLVASQYKIA-PEKLMTGSYSGPSMP-----Q 1437

Qy 88 GLQLALEGISPELGPTLTDLTDVDADFTATTIQQOOMEELGMAPALQPOTQGAMPAFASAFOR 147
Db | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
 | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1438 GLASKMQAASLPQMKNSELKLOEPAQAQHLMQOMAAAMSAAMQOOQ-----VAQAQQQ 1492

Qy 148 RAGGVLVASHLQSFLFSVSRYVLRLHLAQ 174
Db ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1493 AQQAQQAOHQHQQAQOHQLQOQHHLAQ 1519

RESULT 15
F83292
probable sensor/response regulator hybrid PA2824 [imported] - Pseudomonas aeruginosa (str.
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: F83292
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br.
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
. ; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A>Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A;Reference number: AB2950; UID:20437337; PMID:10984043
A;Accession: F83292
A>Status: preliminary
A;Molecule type: DNA
A;Residues: 1-786 <STO>
A/Cross-references: UNIPROT:Q91019; GB:AE004709; GB:AE004091; NID:g9948904; PIDN:AAG0621
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA2824

Query Match 9.5%; Score 85.5; DB 2; Length 786;
Best Local Similarity 28.7%; Pred. No. 4.6;
Matches 49; Conservative 20; Mismatches 49; Indels 53; Gaps 10;

Qy 27 GDGAALQERLC-AIVRLCPBELVLLG--HSLGIWPAPLSGCCPSQAIQLAG-CLSLHSHS 82
Db | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
 | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
490 GLGLALTKEUCEANQGETVVESTVGSLFSVGLPLVPSP-PLQALPLGRVIAQCSAN 548

Qy 83 LFYQGLLQALLEGISPE-----LGPTLDTLQDVLADVATTTTQQMEELGMA 128
Db ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
549 ----SGLAQILQTWLPRMGLEYKRLETDDSLGHSLDVLTSDCPDCL-----MGLR 595

Qy 129 PALOPTQGMPPAFASAFRRAGGVLVASHLQSFL--EVSYRV--LRHLAOP 175
Db | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
596 PSI-----GTPILLVTAYGSFLPELARRLSPQLARP 629

Search completed: December 27, 2004, 13:12:09
Job time : 18 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 13:11:24 ; Search time 63.5 Seconds

(without alignments)
1585.678 Million cell updates/sec

Title: 10032108-2EDIT

Perfect score: 901

Sequence: 1 MTPLGASLPQSFLRLCLE.....SHLQSFLEYSYVRLRLAQP 175

-Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	887	98.4	200	2	Q8N4W3
2	875.5	97.2	207	1	CSF3 HUMAN
3	741	82.2	194	1	CSF3 FELCA
4	741	82.2	195	2	Q9GJU0
5	736	81.7	175	1	CSF3 CANFA
6	735	81.6	174	1	CSF3 SHEEP
7	724	80.4	195	1	CSF3 BOVIN
8	699	77.6	195	1	CSF3 PIG
9	636	70.6	208	1	CSF3 MOUSE
10	629	69.8	214	2	P97712
11	511	56.7	127	2	Q8MKE0
12	301	33.4	201	1	MGF_CHICK
13	109	12.1	241	2	Q90Y10
14	107.5	11.9	212	2	Q8MJ75
15	106	11.8	208	2	Q9XT80
16	103.5	11.5	212	1	IL6 PIG
17	99	11.0	205	1	IL6_ORCOR
18	95	10.5	208	1	IL6_HORSE
19	94.5	10.5	455	2	Q8D706
20	94	10.4	345	2	Q9KTL6
21	92	10.2	189	2	Q6N282
22	92	10.2	189	2	Q9H2A5
23	92	10.2	189	2	AAH66267
24	91	10.1	208	1	IL6 FELCA
25	90.5	10.0	1931	2	Q8RJY3
26	89	9.9	189	2	Q9NPF7
27	89	9.9	189	2	AAH66268
28	89	9.9	189	2	AAQ89442
29	89	9.9	189	2	AAH67511
30	89	9.9	189	2	AAH67512
31	89	9.9	189	2	AAH67513

32	89	9.9	502	2	Q34008
33	89	9.9	788	2	Q8CF87
34	89	9.9	850	2	Q7TQ21
35	89	9.9	851	2	Q8CF88
36	89	9.9	852	2	Q811T9
37	88.5	9.8	666	2	Q9A523
38	87	9.7	189	2	Q6NZ80
39	87	9.7	189	2	AAH66269
40	87	9.7	290	2	Q9P0S7
41	86.5	9.6	214	2	Q8MKES
42	86.5	9.6	2175	1	HMCU DROME
43	85.5	9.5	503	2	Q6D3M5
44	85.5	9.5	786	2	Q9I019
45	85	9.4	193	2	Q9N2H9

ALIGNMENTS

RESULT 1

Q8N4W3	PRELIMINARY;	PRT;	200 AA.
AC	Q8N4W3		
DT	01-OCT-2002 (TremblRel. 22, Created)		
DT	01-OCT-2002 (TremblRel. 22, Last sequence update)		
DT	01-MAR-2004 (TremblRel. 26, Last annotation update)		
DE	Colony stimulating factor 3, isoform c.		
GN	Name=CSF3;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Skin;		
RX	MEDLINE=22388957; PubMed=12477932;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,		
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.		
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,		
RA	Jones S.J., Marra M.A.		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Skin;		
RA	Strausberg R.L.		
RL	Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC033245; AAH33245.1; --		
DR	HSSP; P09919; 1GNC.		
DR	GO; GO:0005576; C:extracellular; IEA.		
DR	GO; GO:0005125; F:cytokine activity; IEA.		
DR	GO; GO:0005138; F:interleukin-6 receptor binding; IEA.		
DR	GO; GO:0006955; P:immune response; IEA.		
DR	InterPro; IPR009079; 4 helix cytokine.		
DR	InterPro; IPR003629; GCSF MGF.		
DR	InterPro; IPR003573; IL6 MGF GCSF.		
DR	InterPro; IPR003574; Interleukin_6.		
DR	Pfam; PF00489; IL6; 1.		
DR	PRINTS; PR00433; IL6GCSFMGF.		

Q34008	beta vulgar
Q8CF87	mus musculus
Q7TQ21	mus musculus
Q8CF88	mus musculus
Q811T9	mus musculus
Q9A523	caulobacter
Q6NZ80	homo sapien
AAH66269	homo sapi
Q9P0S7	homo sapien
Q8MKES	sus scrofa
P10180	drosophila
Q6D3M5	erwinia car
Q9I019	pseudomonas
Q9N2H9	sus scrofa

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DR PRINTS; PR00434; INTERLEUKIN6.
DR ProDom; PD008388; GCSF MGF; 1.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
SQ SEQUENCE 200 AA; 21543 MW; 8648A55B329A96C CRC64;

Query Match          98.4%; Score 887; DB 2; Length 200;
Best Local Similarity 98.3%; Pred. No. 2.2e-72;
Matches 171; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 TPLGPASSLPQSFLRLCQLGQVRIQGDGAALQRLCATYRLCHPELVILGHSLGIPWAP 61
   |||||
DB 27 TPLGPASSLPQSFLRLCQLGQVRIQGDGAALQRLCATYRLCHPELVILGHSLGIPWAP 86
   |||||

QY 62 LSSCPQALQACLSQLHSLGLYQGLLQALGSLPELGPTLDTQLQDVADPATTIWOQ 121
   |||||
DB 87 LSSCPQALQACLSQLHSLGLYQGLLQALGSLPELGPTLDTQLQDVADPATTIWOQ 146
   |||||

QY 122 MEELGNAPALOPTQGAMPAPAFASAFQRRAGGVLVASHLQSFLEYSYRVLRHLAQP 175
   |||||
DB 147 MEELGNAPALOPTQGAMPAPAFASAFQRRAGGVLVASHLQSFLEYSYRVLRHLAQP 200
   |||||

RESULT 2
ID_CSF3 HUMAN STANDARD; PRT; 207 AA.
AC P09919;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DE 01-OCT-2004 (Rel. 45, Last annotation update)
DE Granulocyte colony-stimulating factor precursor (G-CSF) (Pluripoietin)
DE (Filgrastim) (Lenograstim).
GN Name-CSF3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86118679; PubMed=3484805;
RA Nagata S., Tsuchiya M., Asano S., Kaziro Y., Yamazaki T., Yamamoto O.,
RA Hirata Y., Kubota N., Oheda M., Nomura H., Ono M.;
RT "Molecular cloning and expression of cDNA for human granulocyte
RT colony-stimulating factor.";
RL Nature 319:415-418 (1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86220137; PubMed=2423327;
RA Nagata S., Tsuchiya M., Asano S., Yamamoto O., Hirata Y., Kubota N.,
RA Oheda M., Nomura H., Yamazaki T.;
RT "The chromosomal gene structure and two mRNAs for human granulocyte
RT colony-stimulating factor.";
RL EMBO J. 5:575-581 (1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=87196936; PubMed=3494801;
RA Devlin J.J., Devlin P.E., Myambo K., Lilly M.B., Rado T.A.,
RA Warren M.K.;
RT "Expression of granulocyte colony-stimulating factor by human cell
RT lines.";
RN [4]
RP SEQUENCE FROM N.A., AND VARIANTS MET-157 AND THR-174.
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA Nickerson D.A.;
RT "SeattlesNP. NHLBI HL66682 program for genomic applications, UW-
RT FHCR, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 19-207 FROM N.A.
RX MEDLINE=86151684; PubMed=2420009;
RA Souza L.M., Boone T.C., Gabrilove J., Lai P.H., Zsebo K.M.,
RA
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RA Murdock D.C., Chazin V.R., Bruszewski J., Lu H., Chen K.K.,
RA Barendt J., Platzer E., Moore M.A.S., Mettelmann R., Welte K.;
RT "Recombinant human granulocyte colony-stimulating factor: effects on
RT normal and leukemic myeloid cells.";
RL Science 232:61-66 (1986).
RN [6]
RP CARBOHYDRATE-LINKAGE SITE.
RX MEDLINE=93293942; PubMed=7685769;
RA Clogston C.L., Hu S., Boone T.C., Lu H.S.;
RT "Glycosidase digestion, electrophoresis and chromatographic analysis
RT of recombinant human granulocyte colony-stimulating factor glycoforms
RT produced in Chinese hamster ovary cells.";
RL J. Chromatogr. A 637:55-62 (1993).
RN [7]
RP STRUCTURE BY NMR.
RX MEDLINE=93106200; PubMed=1281794;
RA Zink T., Ross A., Ambrosius D., Rudolph R., Holak T.A.;
RT "Secondary structure of human granulocyte colony-stimulating factor
RT derived from NMR spectroscopy.";
RL FEBS Lett. 314:435-439 (1992).
RN [8]
RP STRUCTURE BY NMR.
RX MEDLINE=94304859; PubMed=7518249;
RA Zink T., Ross A., Luers K., Cieslar C., Rudolph R., Holak T.A.;
RT "Structure and dynamics of the human granulocyte colony-stimulating
RT factor determined by NMR spectroscopy. Loop mobility in a four-helix-
RT bundle protein.";
RL Biochemistry 33:8453-8463 (1994).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=93281718; PubMed=7685117;
RA Hill C.P., Oselund T.D., Eisenberg D.;
RT "The structure of granulocyte-colony-stimulating factor and its
RT relationship to other growth factors.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:5167-5171 (1993).
CC -!- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
CC cytokines that act in hematopoiesis by controlling the production,
CC differentiation, and function of 2 related white cell populations
CC of the blood, the granulocytes and the monocytes-macrophages. This
CC CSF induces granulocytes.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=P09919-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=P09919-2; Sequence=VSP_002673;
CC -!- PTM: O-glycan consists of Gal-GalNAc disaccharide which can be
CC modified with up to two sialic acid residues (done in
CC recombinantly expressed G-CSF from CHO cells).
CC -!- PHARMACEUTICAL: Available under the names Neupogen or Granulokine
CC (Amgen/Roche) and Granocyte (Rhône-Poulenc). Used to treat
CC neutropenia (a disorder characterized by an extremely low number
CC of neutrophils in blood).
CC -!- SIMILARITY: Belongs to the IL-6 superfamily.
CC -!- CAUTION: Ref.4 misquotes the gene name as "CSF1".
CC -!- DATABASE: NAME=Neupogen/Granulokine;
CC NOTE=Clinical information on Neupogen/Granulokine;
CC WWW="http://www.neupogen.com/".
CC
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CC
CC EMBL; X03438; CAA27168.1; -
CC EMBL; M13008; AAA03056.1; -
CC EMBL; X03656; CAA27291.1; -
CC EMBL; X03655; CAA27290.1; -
CC
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DR EMBL: AF388025; AAK62469.1; -.
DR EMBL: M17706; AAA35882.1; -.
DR PIR: A24573; A24573.
DR PIR: A25093; FQUGL.
DR PDB: 1CD9; X-ray; A/C=30-207.
DR PDB: 1GNC; NMR; @=30-207.
DR PDB: 1PGR; X-ray; A/C/E/G=30-207.
DR PDB: 1RHG; X-ray; A/B/C=31-207.
DR Genew; HGNC:2438; CSF3.
DR MIM; 138970; -.
DR GO: GO:0005615; C:extracellular space; TAS.
DR GO: GO:0005130; F:granulocyte colony-stimulating factor recep. . .; TAS.
DR GO: GO:0007275; P:development; TAS.
DR GO: GO:0008284; P:positive regulation of cell proliferation; TAS.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR003629; GCSF_MGF.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR ProDom; PD008388; GCSF_MGF; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW 3D-structure: Alternative splicing; Cytokine; Glycoprotein;
KW Growth factor; Pharmaceutical; Polymorphism; Signal.
FT SIGNAL 1 30 Granulocyte colony-stimulating factor.
FT CHAIN 31 207
FT DISULFID 69 75
FT DISULFID 97 107
FT CARBOHYD 166 166
FT VARSPIC 66 68
FT VARIANT 157 157 L -> M (in dbSNP:2227329).
FT VARIANT 174 174 A -> T (in dbSNP:2227330).
FT HELIX 41 65
FT HELIX 69 71
FT HELIX 77 86
FT TURN 87 88
FT HELIX 105 124
FT TURN 125 127
FT TURN 130 132
FT TURN 133 156
FT TURN 157 158
FT HELIX 176 203
FT TURN 204 204
SQ SEQUENCE 207 AA; 22293 MW; 421F635ECCT776996 CRC64;
Query Match 97.2%; Score 875.5; DB 1; Length 207;
Best Local Similarity 96.6%; Pred. No. 2.5e-71;
Matches 171; Conservative 3; Mismatches 0; Indels 3; Gaps 1;
QY 2 TPLGPASSLPQSFLRLCLQVRIQGDGAALQERL---CATYRLCHPELVLLGHSLGIP 58
DB 31 TPLGPASSLPQSFLRLCLQVRIQGDGAALQERLSECATYKLCHEPELVLLGHSLGIP 90
QY 59 WAPLSSCPQALQACLSQLHSGFLYQGLLQALLEGISPELGPTLDTLQLDVADPATTI 118
DB 91 WAPLSSCPQALQACLSQLHSGFLYQGLLQALLEGISPELGPTLDTLQLDVADPATTI 150
QY 119 WQMEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVRLHQAQ 175
DB 151 WQMEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVRLHQAQ 207
RESULT 3
ID CSF3_FELCA STANDARD; PRT; 194 AA.
AC 002708;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Granulocyte colony-stimulating factor precursor (G-CSF) (Fragment).
GN Name-CSF3;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=European shorthair; TISSUE=Lung;
RA MEDLINE=21389237; PubMed=11497496; DOI=10.1006/cyto.2001.0910;
RX Dunham S.P., Onions D.E.;
RT "Isolation, nucleotide sequence and expression of a cDNA encoding
feline granulocyte colony-stimulating factor.";
RL Cytokine 14:347-351(2001).
CC -!- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
cytokines that act in hematopoiesis by controlling the production,
differentiation, and function of 2 related white cell populations
of the blood, the granulocytes and the monocytes-macrophages. This
CSF induces granulocytes (By similarity).
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: O-glycosylated (By similarity).
CC -!- SIMILARITY: Belongs to the IL-6 superfamily.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
EMBL: Y08558; CAA69853.1; -.
DR PIR; T09255; T09255.
DR HSP; P09919; 1RHG.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR003629; GCSF_MGF_GCSF.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR ProDom; PD008388; GCSF_MGF; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT NON_TER 1
FT SIGNAL <1 20 Potential.
FT CHAIN 21 194 Granulocyte colony-stimulating factor.
FT DISULFID 56 62 By similarity.
FT DISULFID 84 94 By similarity.
FT CARBOHYD 153 153 O-linked (GalNAc...) (By similarity).
SQ SEQUENCE 194 AA; 21154 MW; F72B7AB3DAE7385E CRC64;
Query Match 82.2%; Score 741; DB 1; Length 194;
Best Local Similarity 80.5%; Pred. No. 3.8e-59;
Matches 140; Conservative 12; Mismatches 22; Indels 0; Gaps 0;
QY 2 TPLGPASSLPQSFLRLCLQVRIQGDGAALQERLCAVRLCHPELVLLGHSLGIPWAP 61
DB 21 TPLGPTSSLPQSFLRLCLQVRIQGDGAALQERLCAVRLCHPELVLLGHSLGIPQAP 80
QY 62 LSSCPSQALQALQACLSQLHSGFLYQGLLQALLEGISPELGPTLDTLQLDVADPATTI 121
DB 81 LSSCPSQALQALQACLSQLHSGFLYQGLLQALLEGISPELGPTLDTLQLDVADPATTI 140
QY 122 MEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVRLHQAQ 175
DB 141 MEDVGNAPAVPPTQGTMTFTTSAFORRAGGVLVASHLQSFLEVSRYVRLHQAQ 194
RESULT 4
Q9GUUO PRELIMINARY; PRT; 195 AA.
ID Q9GUUO
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Q9GUU0;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Granulocyte colony-stimulating factor precursor.
GN Name-G-CSF;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
[1]
RN MEDLINE=21531548; PubMed=11675019;
RX Yamamoto A., Iwata A., Tuchiya K., Katsumata A., Oishi K., Saito T.,
RA Teujimoto H., Hasegawa A., Ueda S.;
RT "Molecular cloning and expression of the cDNA encoding feline
granulocyte colony-stimulating factor.";
RL Gene 274:263-269 (2001).
DR EMBL; AB042552; BAB17789.1; -.
DR HSSP; AB042553; BAB17757.1; -.
DR HSSP; P09919; IAHG.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR003629; GCSF_MGF.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN_6.
DR ProDom; PD008388; GCSF_MGF; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 195 AA; 21255 MW; 544C682909412PCF CRC64;
Query Match 82.2%; Score 741; DB 2; Length 195;
Best Local Similarity 80.5%; Pred. No. 3.8e-59;
Matches 140; Conservative 12; Mismatches 22; Indels 0; Gaps 0;
Qy 2 TPLGPASSLPQSFLRLCQLQVQRKIQGGAAALQERLCATYRLCHPEELVLLGHSLGIPWAP 61
Db 22 TPLGTSLSLPQSFLRLCQLQVQRKIQGGAAALQERLCATYRLCHPEELVLLGHSLGIPWAP 81
Qy 62 LSSCPQALQALAGCLSQLHSLGLFLYQGLLQALAGISPELGFTLDTLQLDVADFAATTIWOQ 121
Db 82 LSSCSQALQALQTLGCLRLQHLHSLGLFLYQGLLQALAGISPELAPTLDMLQDLITDFAINIWOQ 141
Qy 122 MEELGMALOPTQGMAPAFASAFORRAGGVLVASHLQSFLEVSRYVRLHLAQP 175
Db 142 MEDVGMAPVPTQGTMTPTFTSAFORRAGGVLVASHLQSFLEVSRYVRLHLAQP 195
RESULT 5
CSF3_CANFA STANDARD; PRT; 175 AA.
AC P35834;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Granulocyte colony-stimulating factor (G-CSF).
GN Name=CSF3;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RX MEDLINE=94076341; PubMed=7504736;
RA Lovejoy B., Cascio D., Eisenberg J.;
RT "Crystal structure of canine and bovine granulocyte-colony stimulating factor (G-CSF).";
RL J. Mol. Biol. 234:640-653 (1993).
CC -!- FUNCTION: Granulocyte/macrophage colony-stimulating factors are cytokines that act in hematopoiesis by controlling the production, differentiation, and function of 2 related white cell populations of the blood, the granulocytes and the monocytes-macrophages. This CSF induces granulocytes.
CC -!- SURUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-6 superfamily.
DR PDB; 1BGD; X-ray; @=1-175.
DR PDB; 1BGE; X-ray; A/B=1-175.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR003629; GCSF_MGF.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR ProDom; PD008388; GCSF_MGF; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW 3D-structure; Cytokine; Glycoprotein; Growth factor.
FT DISULFID 37 43
FT DISULFID 65 75
FT CARBOHYD 134 134
FT STRAND 10 10
FT HELIX 12 39
FT HELIX 45 55
FT TURN 56 56
FT TURN 63 65
FT TURN 67 69
FT TURN 72 92
FT TURN 93 95
FT TURN 98 100
FT TURN 101 125
FT TURN 126 126
FT TURN 144 171
FT TURN 172 172
FT STRAND 173 173
SQ SEQUENCE 175 AA; 18858 MW; 28C26B24990C6DB3 CRC64;
Query Match 81.7%; Score 736; DB 1; Length 175;
Best Local Similarity 80.0%; Pred. No. 9.6e-59;
Matches 140; Conservative 12; Mismatches 23; Indels 0; Gaps 0;
Qy 1 MTPLGASSLPQSFLRLCQLQVQRKIQGGAAALQERLCATYRLCHPEELVLLGHSLGIPWA 60
Db 1 MAPLGFTGFLPQSFLRLCQLQVQRKIQGGAAALQERLCATYRLCHPEELVLLGHSLGIPQP 60
Qy 61 PLSSCPQALQALAGCLSQLHSLGLFLYQGLLQALAGISPELGFTLDTLQLDVADFAATTIWO 120
Db 61 PLSSCSQALQALQTLGCLRLQHLHSLGLFLYQGLLQALAGISPELAPTLDMLQDLITDFAINIWO 120
Qy 121 QMEELGMALOPTQGMAPAFASAFORRAGGVLVASHLQSFLEVSRYVRLHLAQP 175
Db 121 QMEDLGMAPVPTQGTMTPTFTSAFORRAGGVLVASHLQSFLEVSRYVRLHLAQP 175
RESULT 6
CSF3_SHEEP STANDARD; PRT; 174 AA.
AC Q28746;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Granulocyte colony-stimulating factor (G-CSF).
GN Name=CSF3;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OX NCBI_TaxID=9940;


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[1]
RP MEDLINE=95102116; PubMed=7528579;
RA "Brien P.M., Seow H.P., Rothel J.S., Wood P.R.;
RT "Cloning and sequencing of an ovine granulocyte colony-stimulating
RT factor cDNA.";
RL DNA Seq. 4:339-342(1994).
CC -1- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
CC cytokines that act in hematopoiesis by controlling the production,
CC differentiation, and function of 2 related white cell populations
CC of the blood, the granulocytes and the monocytes-macrophages. This
CC CSF induces granulocytes (By similarity).
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: O-glycosylated (By similarity).
CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
EMBL; L07939; AAA68006.1; -.
DR PIR; T10268; T10268.
DR HSSP; P09919; 1RHG.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR003629; GCSF_MGF.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR ProDom; PD008388; GCSF_MGF; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR Cytokine; Glycoprotein; Growth factor.
DR DISULFID 36 42 By similarity.
FT DISULFID 64 74 By similarity.
FT CARBOHYD 133 133 O-linked (GalNAc...) (By similarity).
SQ SEQUENCE 174 AA; 18806 MW; BA5AA8F8D23ACD1E CRC64;

Query Match 81.6%; Score 735; DB 1; Length 174;
Best Local Similarity 81.6%; Pred. No. 1.2e-58;
Matches 142; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

QY 2 TPLGPASSLPQSFLRLCQVRKIQDGAALQERLCATYRLCHPELVLLHSLGIPWAP 61
Db 1 TPLGPARSUPQSFLKCLQVRKIQDGAELQERLCATKCHPELVLLHSLGIPQAP 60

QY 62 LSSCPQALQAGCLSQLHSLFLYQGLLQALGSLPELPTLDTLQLDVADPATTIWOQ 121
Db 61 LSSCSSQSLLTSCDLQHLGFLYQGLLQALAGISPELAPTLDLTLDVDFATNIWLQ 120

QY 122 MEELGWAPALQPTQAMPAPASAFORRAGVLVASHLQSFLEVSIVRLHLAQP 175
Db 121 MEDLGVAPAVQPTQGTMTFTSAFORRAGVLVASQLRFLGLAYRGLYLAEP 174

RESULT 7
CSF3_BOVIN STANDARD; PRT; 195 AA.
ID CSF3_BOVIN
AC P35833; Q9TV89;
DT 01-JUN-1994 (Rel. 29, Created)
DT 15-OCT-2001 (Rel. 40, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Granulocyte colony-stimulating factor precursor (G-CSF).
GN Names=CSF3; Synonyms=GCSF;
OS Bos taurus (Bovine).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OC NCBI_TaxID=9913;
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[1]
RP SEQUENCE FROM N.A.
RC STRAIN=Holstein;
RA Heidari M., Kehrli M.E. Jr.;
RT "Cloning, sequencing, and analysis of cDNA encoding bovine granulocyte
RT colony stimulating factor.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
[2]
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
RX MEDLINE=94076341; PubMed=7504736;
RA Lovejoy B., Cascio D., Eisenberg D.;
RT "Crystal structure of canine and bovine granulocyte-colony stimulating
RT factor (G-CSF).";
RL J. Mol. Biol. 234:640-653(1993).
CC -1- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
CC cytokines that act in hematopoiesis by controlling the production,
CC differentiation, and function of 2 related white cell populations
CC of the blood, the granulocytes and the monocytes-macrophages. This
CC CSF induces granulocytes.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: O-glycosylated.
CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
EMBL; AF092533; AAD16102.1; -.
DR PDB; 1BGC; X-ray; @=22-195.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR003629; GCSF_MGF.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR ProDom; PD008388; GCSF_MGF; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR 3D-structure; Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 195 Granulocyte colony-stimulating factor.
FT DISULFID 57 63
FT DISULFID 85 95
FT CARBOHYD 154 154
FT CONFLICT 93 94
FT HELIX 32 60
FT HELIX 65 69
FT TURN 70 71
FT TURN 72 75
FT TURN 76 76
FT HELIX 83 85
FT TURN 87 89
FT HELIX 92 112
FT TURN 113 115
FT TURN 118 120
FT HELIX 121 145
FT HELIX 164 191
FT TURN 192 192
SQ SEQUENCE 195 AA; 21431 MW; 8C06119E4ADFBA73 CRC64;

Query Match 80.4%; Score 724; DB 1; Length 195;
Best Local Similarity 80.5%; Pred. No. 1.3e-57;
Matches 140; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

QY 2 TPLGPASSLPQSFLRLCQVRKIQDGAALQERLCATYRLCHPELVLLHSLGIPWAP 61
Db 22 TPLGPARSUPQSFLKCLQVRKIQDGAELQERLCATKCHPELVLLHSLGIPQAP 81

QY 62 LSSCPQALQAGCLSQLHSLFLYQGLLQALGSLPELPTLDTLQLDVADPATTIWOQ 121
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Db 82 LSCSSQSLQSLNQLHGGFLYQGLLQALAGISPELAPLDTLTLQDVTDFATNIWLQ 141
QY 122 MEELGNAPALQPTQGAMPAPASAFORRAGGVLVASHLQSLFVSVTVRLHQAOP 175
Db 142 MEDLGAAPVQPTQGAMPPTFTSAFORRAGGVLVASQLHRFLELAVRGLFYLAEP 195

RESULT 8

CSF3_PIG STANDARD; PRT; 195 AA.
AC O02837; 019180;
DT 15-JUL-1998 (Rel. 36, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Granulocyte colony-stimulating factor precursor (G-CSF).
GN Names=CSF3;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9623;
[1]
RP SEQUENCE FROM N.A.
RA Kulmburg P.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Gloster S.E., Sandeman R.M., Strom A.D.G.;
RT "Cloning of a cDNA and gene encoding porcine granulocyte-colony
stimulating factor.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
cytokines that act in hematopoiesis by controlling the production,
differentiation, and function of 2 related white cell populations
of the blood, the granulocytes and the monocytes-macrophages. This
CSF induces granulocytes (By similarity).
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: O-glycosylated (By similarity).
CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
CC
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CC
CC EMBL; Y10494; CAA71518.1; -
CC EMBL; U68482; AAB70701.1; -
CC EMBL; U68481; AAB70700.1; -
CC HSSP; P09919; IRRG.
CC InterPro; IPR009079; 4_helix_cytokine.
CC InterPro; IPR003629; GCSF_MGF.
CC InterPro; IPR003573; IL6_MGF_GCSF.
CC Pfam; PF00489; IL6; 1
CC PRINTS; PR00433; IL6GCSFMGF.
CC ProDom; PD008388; GCSF_MGF; 1.
CC SMART; SM00126; IL6; 1.
CC PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 195 Granulocyte colony-stimulating factor.
FT DISULFID 57 63 By similarity.
FT DISULFID 85 95 By similarity.
FT CARBOHYD 154 154 O-linked (GalNAc...) (By similarity).
FT CONFLICT 123 123 A -> R (in Ref. 1).
SQ SEQUENCE 195 AA; 21214 MW; 84787E20DB0BAE1C CRC64;
Query Match 77.6%; Score 699; DB 1; Length 195;
Best Local Similarity 78.6%; Pred. No. 2.5e-55;

Matches 136; Conservative 12; Mismatches 25; Indels 0; Gaps 0;
QY 3 PLGPASSLPQSFLRLCLQEQVRKIQDGAALQERLCATYRLCHPEELVLLGHSLGIPWAPL 62
Db 23 PLGPASSLPQSFLRLCLQEQVRKIQDGAALQERLCATYRLCHPEELVLLGHSLGIPWAPL 82
QY 63 SSCPSQALQALAGCISLQSLHGLFLYQGLLQALAGISPELAPLDTLTLQDVTDFATNIQOM 122
Db 83 SSCPSQALQALAGCISLQSLHGLFLYQGLLQALAGISPELAPLDTLTLQDVTDFATNIQOM 142
QY 123 EELGNAPALQPTQGAMPAPASAFORRAGGVLVASHLQSLFVSVTVRLHQAOP 175
Db 143 EDLRNAPASLPTQGTVPFTTSAFORRAGGVLVASHLQSLFVSVTVRLHQAOP 195

RESULT 9

CSF3_MOUSE STANDARD; PRT; 208 AA.
AC P09920;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Granulocyte colony-stimulating factor precursor (G-CSF).
GN Name=Csf3; Synonyms=Csf3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RA MEDLINE=87017003; PubMed=3489940;
RT "Isolation and characterization of the cDNA for murine granulocyte
colony-stimulating factor.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:7633-7637(1986).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=87190474; PubMed=3494605;
RT "The chromosomal gene structure for murine granulocyte colony-
stimulating factor.";
RL Eur. J. Biochem. 165:7-12(1987).
RN [3]
RP PARTIAL SEQUENCE.
RA Simpson R.J., Nice E.C., Nicola N.A.;
RT "Structural studies on the murine granulocyte colony-stimulating
factor.";
RL Biol. Chem. Hoppe-Seyler 368:1327-1331(1987).
CC -1- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
cytokines that act in hematopoiesis by controlling the production,
differentiation, and function of 2 related white cell populations
of the blood, the granulocytes and the monocytes-macrophages. This
CSF induces granulocytes.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: O-glycosylated (By similarity).
CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
CC
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CC
CC EMBL; M13926; AAA37672.1; -
CC EMBL; X05402; CAA28986.1; -
CC PIR; A29536; A26496.
CC HSSP; P09919; IRRG.
CC MGI; MGI:1339751; Csf3.
CC InterPro; IPR009079; 4_helix_cytokine.
CC


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OC Archosauaria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92231616; PubMed=2785450;
RA Leutz A., Damm K., Sterneck E., Kowenz E., Ness S., Frank R.,
RA Gausepohl H., Pan Y.-C.E., Smart J., Hayman M., Graf T.;
RT "Molecular cloning of the chicken myelomonocytic growth factor (CMGF)
RT reveals relationship to interleukin 6 and granulocyte colony
RT stimulating factor.";
RL EMBO J. 8:175-181(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92195319; PubMed=1549124;
RA Sterneck E., Blattner C., Graf T., Leutz A.;
RT "Structure of the chicken myelomonocytic growth factor gene and
RT specific activation of its promoter in avian myelomonocytic cells by
RT protein kinases.";
RL Mol. Cell. Biol. 12:1728-1735(1992).
CC -!- FUNCTION: Hematopoietic growth factor that stimulates the
CC proliferation and colony formation of normal and transformed avian
CC cells of the myeloid lineage.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-6 superfamily.
CC -----
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CC -----
DR EMBL; M85034; AAA48694.1; -;
DR EMBL; X14477; CAA32639.1; -;
DR PIR; A42247; A42247.
DR HSSP; P09919; LRHG.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR003629; GCSF MGF.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN6.
DR ProDom; PD008388; GCSF MGF; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 23
FT CHAIN 24 201 Myelomonocytic growth factor.
FT DISULFID 61 67 By similarity.
FT DISULFID 89 99 By similarity.
FT CARBOHYD 123 123 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 137 137 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 201 AA; 240A8DD21B4244E6 CRC64;
Query Match 33.4%; Score 301; DB 1; Length 201;
Best Local Similarity 40.0%; Pred. No. 3.3e-19; Mismatches 68; Indels 2; Gaps 1;
Matches 66; Conservative 29;
QY 12 QSFLLRCLEQVRKIQDGAALQRLCATYRLCHPEELVLIGHSLGIPWAPLSLSCPSQALQ 71
DB 36 QLFELHKNLEFTRKIRGDVAALQRAVCDTFLCTEELQLVQPPHVLVQAPLQDCKRGQ 95
QY 72 LAGCLSQLHSLGLYQGLQALREGISPELGPDTLDLTOLDVADPATTIWOQMEELGNAPAL 131
DB 96 AEVCFQIRAGLHAYHDSGLAVRLLEPHNTTLVETLQDAANLSNIQQOMEDLGLDVT 155
QY 132 QPTQ--GAMPAPAFASFORAGGVLVASHLQSFLEVSRYVLRHLAQ 174
DB 156 LPAEQSPPTFTSGPPQQVGGFFILANFORFLETAIRLHAR 200
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RESULT 13
Q90YIO PRELIMINARY; PRT; 241 AA.
ID Q90YIO;
AC Q90YIO;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Interleukin-6 precursor.
GN Name=IL-6;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauaria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Schneider K., Klaas R., Kaspers B., Staeheli P.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Kaiser P., Rothwell L., Galyov E.E., Barrow P.A., Burnside J.,
RA Wigley P.;
RT "Differential cytokine expression in avian cells in response to
RT invasion by Salmonella typhimurium, Salmonella enteritidis and
RT Salmonella gallinarum.";
RL Microbiology 146:3217-3226(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Kaiser P.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ309540; CAC40812.1; -;
DR EMBL; AJ250838; CAC15566.2; -;
DR HSSP; P05231; 1ALU.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR003629; GCSF MGF.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN6.
DR ProDom; PD008388; GCSF MGF; 1.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Signal.
FT SIGNAL 1 47 Potential.
FT CHAIN 48 241 mature CHIL-6.
SQ SEQUENCE 241 AA; 26790 MW; 657F8049F25BD2F8 CRC64;
Query Match 12.1%; Score 109; DB 2; Length 241;
Best Local Similarity 22.2%; Pred. No. 0.11;
Matches .46; Conservative 34; Mismatches 75; Indels 52; Gaps 7;
QY 4 LCPASSLP-----QSFILRCLEQVRKIQDGAALQRLCATYRLCH 44
DB 41 LPFAAVPLPAAADSSEGVLEEGAGARALLDCBFLARVLRDRVQLQDEWCKKFTVCE 100
QY 45 PEELVLIGHSLGIPWAPLSLSCPSQALQALAG-----CLSQLHSLGLYQGLQALREGISPE 99
DB 101 NSMEMLVRNNINLP----KVTEEDGCLLAGPDEEKCLTKLSGLFAFQYLFQIETFDS 156
QY 100 LGFTLDLTOLDVADPATTIWOQMEELGNAPALQPTQGAMPAPAFASFORAGGV 153
DB 157 EQNVEESLCYSTKHLAATIRQWV-----INPDEVWIP--DSAAQKSLLANLAKSDKW 206
QY 154 ---VASHL-----QSFLEVSRYVLRHL 172
DB 207 IEKITHLILRDTFTSFMEKTVRAVRYL 233
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OM protein - protein search, using sw model

Run on: December 27, 2004, 13:14:34 ; Search time 297.5 Seconds
(without alignments)
211.245 Million cell updates/sec

Title: 10032108-2EDIT

Perfect score: 901

Sequence: 1 MTPGLPASSLPQSFLRLCLE.....SHLQSFLEVSRYVLRHLAQP 175

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1595201 seqs, 359116952 residues

Total number of hits satisfying chosen parameters: 1595201

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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2:	/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3:	/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
4:	/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5:	/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6:	/cgn2_6/ptodata/2/pubpaa/PCTU5_PUBCOMB.pep.*
7:	/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8:	/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9:	/cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
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12:	/cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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17:	/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18:	/cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19:	/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20:	/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	901	100.0	175	9	US-09-754-532-72
2	901	100.0	175	14	US-10-032-108-72
3	898	99.7	175	9	US-09-754-532-74
4	898	99.7	175	14	US-10-032-108-74
5	895	99.3	175	9	US-09-754-532-67
6	895	99.3	175	9	US-09-754-532-69
7	895	99.3	175	9	US-09-754-532-70
8	895	99.3	175	9	US-09-754-532-71
9	895	99.3	175	9	US-09-754-532-73
10	895	99.3	175	9	US-09-754-532-75
11	895	99.3	175	14	US-10-032-108-67
12	895	99.3	175	14	US-10-032-108-69
13	895	99.3	175	14	US-10-032-108-70
14	895	99.3	175	9	US-09-754-532-72
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67	895	99.3	175	14	US-10-032-108-72
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69	895	99.3	175	14	US-10-032-108-74
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192	895	99.3	175	9	US-09-754-532-75
193	895	99.3	175	14	US-10-032-108-67
194	895	99.3	175	14	US-10-032-108-69
195	895	99.3	175	14	US-10-032-108-70
196	895	99.3	175	9	US-09-754-532-72
197	895	99.3</			

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-754-532-72

Query Match 100.0%; Score 901; DB 9; Length 175;
Best Local Similarity 100.0%; Pred. No. 7.8e-83;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGPASSLPQSFLRLCLQEQVKIQDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
DB 1 MTPLGPASSLPQSFLRLCLQEQVKIQDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
QY 61 PLSSCPSQALQAGLSQLHSGFLYQGLLQALEGISPELGTDLTLDQDVADFATTIQQ 120
DB 61 PLSSCPSQALQAGLSQLHSGFLYQGLLQALEGISPELGTDLTLDQDVADFATTIQQ 120
QY 121 QMEELGNAPALQPTQGMPPAFASAFORRAGGVVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGNAPALQPTQGMPPAFASAFORRAGGVVASHLQSFLEVSRYVLRHLAQP 175

RESULT 2
US-10-032-108-72
; Sequence 72, Application US/10032108
; Publication No. US20030171559A1
; GENERAL INFORMATION:
; APPLICANT: Oselund, Timothy
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; FILE REFERENCE: 01017/38834F
; CURRENT APPLICATION NUMBER: US/10/032,108
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 09/754,532
; PRIOR FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: US 09/304,186
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 09/027,508
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: US 08/956,812
; PRIOR FILING DATE: 1987-10-23
; PRIOR APPLICATION NUMBER: US 08/448,716
; PRIOR FILING DATE: 1995-05-24
; PRIOR APPLICATION NUMBER: US 08/010,099
; PRIOR FILING DATE: 1993-01-28
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: Patent-In ver. 3.1
; SEQ ID NO 72
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Artificial sequence
; OTHER INFORMATION: G-CSF analog
US-10-032-108-72

Query Match 100.0%; Score 901; DB 14; Length 175;
Best Local Similarity 100.0%; Pred. No. 7.8e-83;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGPASSLPQSFLRLCLQEQVKIQDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
DB 1 MTPLGPASSLPQSFLRLCLQEQVKIQDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
QY 61 PLSSCPSQALQAGLSQLHSGFLYQGLLQALEGISPELGTDLTLDQDVADFATTIQQ 120
DB 61 PLSSCPSQALQAGLSQLHSGFLYQGLLQALEGISPELGTDLTLDQDVADFATTIQQ 120
QY 121 QMEELGNAPALQPTQGMPPAFASAFORRAGGVVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGNAPALQPTQGMPPAFASAFORRAGGVVASHLQSFLEVSRYVLRHLAQP 175

RESULT 3
US-09-754-532-74

; Sequence 74, Application US/09754532
; Patent No. US20010016191A1
; GENERAL INFORMATION:
; APPLICANT: Oselund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,532
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-754-532-74

Query Match 99.7%; Score 898; DB 9; Length 175;
Best Local Similarity 99.4%; Pred. No. 1.6e-82;
Matches 174; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGPASSLPQSFLRLCLQEQVKIQDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
DB 1 MTPLGPASSLPQSFLRLCLQEQVKIQDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
QY 61 PLSSCPSQALQAGLSQLHSGFLYQGLLQALEGISPELGTDLTLDQDVADFATTIQQ 120
DB 61 PLSSCPSQALQAGLSQLHSGFLYQGLLQALEGISPELGTDLTLDQDVADFATTIQQ 120
QY 121 QMEELGNAPALQPTQGMPPAFASAFORRAGGVVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGNAPALQPTQGMPPAFASAFORRAGGVVASHLQSFLEVSRYVLRHLAQP 175

RESULT 4
US-10-032-108-74
; Sequence 74, Application US/10032108
; Publication No. US20030171559A1
; GENERAL INFORMATION:
; APPLICANT: Oselund, Timothy
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; FILE REFERENCE: 01017/38834F
; CURRENT APPLICATION NUMBER: US/10/032,108
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 09/754,532
; PRIOR FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: US 09/304,186
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 09/027,508
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: US 08/956,812

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; PRIOR FILING DATE: 1987-10-23
; PRIOR APPLICATION NUMBER: US 08/448,716
; PRIOR FILING DATE: 1995-05-24
; PRIOR APPLICATION NUMBER: US 08/010,099
; PRIOR FILING DATE: 1993-01-28
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: Patent-In ver. 3.1
; SEQ ID NO 74
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: G-CSF analog
US-10-032-108-74

Query Match          99.7%; Score 898; DB 14; Length 175;
Best Local Similarity 99.4%; Pred. No. 1.6e-82;
Matches 174; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPGPASSLPQSFLRLCLCEQVRKIQDGAALQERLCATYRLCHPBEVLVLLGHSGLIPWA 60
DB 1 MTPGPASSLPQSFLRLCLCEQVRKIQDGAALQERLCATYRLCHPBEVLVLLGHSGLIPWA 60
QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPPTLDTLQLDVADFATTIWQ 120
DB 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPPTLDTLQLDVADFATTIWQ 120
QY 121 QMEELGMALPQTOGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGMALPQTOGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 5
US-09-754-532-67
; Sequence 67, Application US/09754532
; Patent No. US20010016191A1
; GENERAL INFORMATION:
; APPLICANT: Oselund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,532
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-754-532-67

Query Match          99.3%; Score 895; DB 9; Length 175;
Best Local Similarity 98.9%; Pred. No. 3.2e-82;
Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPGPASSLPQSFLRLCLCEQVRKIQDGAALQERLCATYRLCHPBEVLVLLGHSGLIPWA 60
DB 1 MTPGPASSLPQSFLRLCLCEQVRKIQDGAALQERLCATYRLCHPBEVLVLLGHSGLIPWA 60
QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPPTLDTLQLDVADFATTIWQ 120
DB 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPPTLDTLQLDVADFATTIWQ 120
QY 121 QMEELGMALPQTOGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGMALPQTOGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 6
US-09-754-532-69
; Sequence 69, Application US/09754532
; Patent No. US20010016191A1
; GENERAL INFORMATION:
; APPLICANT: Oselund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,532
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-754-532-69

Query Match          99.3%; Score 895; DB 9; Length 175;
Best Local Similarity 98.9%; Pred. No. 3.2e-82;
Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPGPASSLPQSFLRLCLCEQVRKIQDGAALQERLCATYRLCHPBEVLVLLGHSGLIPWA 60
DB 1 MTPGPASSLPQSFLRLCLCEQVRKIQDGAALQERLCATYRLCHPBEVLVLLGHSGLIPWA 60
QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPPTLDTLQLDVADFATTIWQ 120
DB 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPPTLDTLQLDVADFATTIWQ 120
QY 121 QMEELGMALPQTOGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGMALPQTOGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
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RESULT 7
US-09-754-532-70
; Sequence 70, Application US/09754532
; Patent No. US20010016191A1
; GENERAL INFORMATION:
; APPLICANT: Osslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Angen Inc.
; STREET: Angen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,532
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-754-532-70

Query Match 99.3%; Score 895; DB 9; Length 175;
Best Local Similarity 98.9%; Pred. No. 3.2e-82;
Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGPASSLPQSFLRLCQLQVRRKIQDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
DB 1 MTPLGPASSLPQSFLRLCQLQVRRKIQDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
QY 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDQDVADFTATIQ 120
DB 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDQDVADFTATIQ 120
QY 121 QMEELGNAPALQPTQGAAPAFASAFORRAGGVLVASHLQSFLEVSRYRVLRLHQAQ 175
DB 121 QMEELGNAPALQPTQGAAPAFASAFORRAGGVLVASHLQSFLEVSRYRVLRLHQAQ 175

RESULT 8
US-09-754-532-71
; Sequence 71, Application US/09754532
; Patent No. US20010016191A1
; GENERAL INFORMATION:
; APPLICANT: Osslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Angen Inc.
; STREET: Angen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
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; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,532
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-754-532-71

Query Match 99.3%; Score 895; DB 9; Length 175;
Best Local Similarity 98.9%; Pred. No. 3.2e-82;
Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGPASSLPQSFLRLCQLQVRRKIQDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
DB 1 MTPLGPASSLPQSFLRLCQLQVRRKIQDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
QY 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDQDVADFTATIQ 120
DB 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDQDVADFTATIQ 120
QY 121 QMEELGNAPALQPTQGAAPAFASAFORRAGGVLVASHLQSFLEVSRYRVLRLHQAQ 175
DB 121 QMEELGNAPALQPTQGAAPAFASAFORRAGGVLVASHLQSFLEVSRYRVLRLHQAQ 175

RESULT 9
US-09-754-532-73
; Sequence 73, Application US/09754532
; Patent No. US20010016191A1
; GENERAL INFORMATION:
; APPLICANT: Osslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Angen Inc.
; STREET: Angen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,532
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
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; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-754-532-73

Query Match      99.3%; Score 895; DB 9; Length 175;
Best Local Similarity 98.9%; Pred. No. 3.2e-82;
Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGPASSLPQSFLRLCLCEQVRKIQGDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
DB 1 MTPLGPASSLPQSFLRLCLCEQVRKIQGDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
QY 61 PLSSCPSQALQAGCLSQLHSGLFLYQGLLQALEGISPELGTDLTDLQDVADFATTIQQ 120
DB 61 PLSSCPSQALQAGCLSQLHSGLFLYQGLLQALEGISPELGTDLTDLQDVADFATTIQQ 120
QY 121 QMEELGMAPALOPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYRLRHLAQP 175
DB 121 QMEELGMAPALOPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYRLRHLAQP 175

RESULT 10
US-09-754-532-75
; Sequence 75, Application US/09754532
; Patent No. US20010016191A1
; GENERAL INFORMATION:
; APPLICANT: Oslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,532
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-754-532-75

Query Match      99.3%; Score 895; DB 9; Length 175;
Best Local Similarity 98.9%; Pred. No. 3.2e-82;
Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGPASSLPQSFLRLCLCEQVRKIQGDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
DB 1 MTPLGPASSLPQSFLRLCLCEQVRKIQGDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
QY 61 PLSSCPSQALQAGCLSQLHSGLFLYQGLLQALEGISPELGTDLTDLQDVADFATTIQQ 120
DB 61 PLSSCPSQALQAGCLSQLHSGLFLYQGLLQALEGISPELGTDLTDLQDVADFATTIQQ 120
QY 121 QMEELGMAPALOPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYRLRHLAQP 175
DB 121 QMEELGMAPALOPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYRLRHLAQP 175

RESULT 11
US-10-032-108-67
; Sequence 67, Application US/10032108
; Publication No. US20030171559A1
; GENERAL INFORMATION:
; APPLICANT: Oslund, Timothy
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; FILE REFERENCE: 01017/38834F
; CURRENT APPLICATION NUMBER: US/10/032,108
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 09/754,532
; PRIOR FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: US 09/304,186
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 09/027,508
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: US 08/956,812
; PRIOR FILING DATE: 1987-10-23
; PRIOR APPLICATION NUMBER: US 08/448,716
; PRIOR FILING DATE: 1995-05-24
; PRIOR APPLICATION NUMBER: US 08/010,099
; PRIOR FILING DATE: 1993-01-28
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: Patent-In ver. 3.1
; SEQ ID NO 67
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: G-CSF analog
US-10-032-108-67

Query Match      99.3%; Score 895; DB 14; Length 175;
Best Local Similarity 98.9%; Pred. No. 3.2e-82;
Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGPASSLPQSFLRLCLCEQVRKIQGDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
DB 1 MTPLGPASSLPQSFLRLCLCEQVRKIQGDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
QY 61 PLSSCPSQALQAGCLSQLHSGLFLYQGLLQALEGISPELGTDLTDLQDVADFATTIQQ 120
DB 61 PLSSCPSQALQAGCLSQLHSGLFLYQGLLQALEGISPELGTDLTDLQDVADFATTIQQ 120
QY 121 QMEELGMAPALOPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYRLRHLAQP 175
DB 121 QMEELGMAPALOPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYRLRHLAQP 175

RESULT 12
US-10-032-108-69
; Sequence 69, Application US/10032108
; Publication No. US20030171559A1
; GENERAL INFORMATION:
; APPLICANT: Oslund, Timothy
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; FILE REFERENCE: 01017/38834F
; CURRENT APPLICATION NUMBER: US/10/032,108
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/ CURRENT FILING DATE: 2003-01-31
/ PRIOR APPLICATION NUMBER: US 09/754,532
/ PRIOR FILING DATE: 2001-01-03
/ PRIOR APPLICATION NUMBER: US 09/304,186
/ PRIOR FILING DATE: 1999-05-03
/ PRIOR APPLICATION NUMBER: US 08/956,812
/ PRIOR FILING DATE: 1998-02-20
/ PRIOR APPLICATION NUMBER: US 08/448,716
/ PRIOR FILING DATE: 1995-05-24
/ PRIOR APPLICATION NUMBER: US 08/010,099
/ PRIOR FILING DATE: 1993-01-28
/ NUMBER OF SEQ ID NOS: 110
/ SOFTWARE: Patent-In ver. 3.1
/ SEQ ID NO 69
/ LENGTH: 175
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: G-CSF analog
US-10-032-108-69

Query Match      99.3%; Score 895; DB 14; Length 175;
Best Local Similarity 98.9%; Pred. No. 3.2e-82;
Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTPLGPASSLPQSFLRLCLQEVKIQDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
Db 1 MTPLGPASSLPQSFLRLCLQEVKIQDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60

Qy 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPPTLDTLQLDVADFATTIQ 120
Db 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPPTLDTLQLDVADFATTIQ 120

Qy 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
Db 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 14
US-10-032-108-71
/ Sequence 71, Application US/10032108
/ Publication No. US20030171559A1
/ GENERAL INFORMATION:
/ APPLICANT: Osslund, Timothy
/ TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
/ FILE REFERENCE: 01017/38834F
/ CURRENT APPLICATION NUMBER: US/10/032,108
/ CURRENT FILING DATE: 2003-01-31
/ PRIOR APPLICATION NUMBER: US 09/754,532
/ PRIOR FILING DATE: 2001-01-03
/ PRIOR APPLICATION NUMBER: US 09/304,186
/ PRIOR FILING DATE: 1999-05-03
/ PRIOR APPLICATION NUMBER: US 09/027,508
/ PRIOR FILING DATE: 1998-02-20
/ PRIOR APPLICATION NUMBER: US 08/956,812
/ PRIOR FILING DATE: 1987-10-23
/ PRIOR APPLICATION NUMBER: US 08/448,716
/ PRIOR FILING DATE: 1995-05-24
/ PRIOR APPLICATION NUMBER: US 08/010,099
/ PRIOR FILING DATE: 1993-01-28
/ NUMBER OF SEQ ID NOS: 110
/ SOFTWARE: Patent-In ver. 3.1
/ SEQ ID NO 71
/ LENGTH: 175
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: G-CSF analog
US-10-032-108-71

Query Match      99.3%; Score 895; DB 14; Length 175;
Best Local Similarity 98.9%; Pred. No. 3.2e-82;
Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTPLGPASSLPQSFLRLCLQEVKIQDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
Db 1 MTPLGPASSLPQSFLRLCLQEVKIQDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60

Qy 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPPTLDTLQLDVADFATTIQ 120
Db 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPPTLDTLQLDVADFATTIQ 120

Qy 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
Db 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 15
US-10-032-108-73
/ Sequence 73, Application US/10032108
/ Publication No. US20030171559A1
/ GENERAL INFORMATION:
/ APPLICANT: Osslund, Timothy
/ TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
/ FILE REFERENCE: 01017/38834F
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; CURRENT APPLICATION NUMBER: US/10/032,108
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 09/754,532
; PRIOR FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: US 09/304,186
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 09/027,508
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: US 08/956,812
; PRIOR FILING DATE: 1987-10-23
; PRIOR APPLICATION NUMBER: US 08/448,716
; PRIOR FILING DATE: 1995-05-24
; PRIOR APPLICATION NUMBER: US 08/010,099
; PRIOR FILING DATE: 1993-01-28
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: Patent-In ver. 3.1
; SEQ ID NO 73
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: G-CSF analog
US-10-032-108-73

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Query Match      99.3%; Score 895; DB 14; Length 175;
Best Local Similarity 98.9%; Pred. No. 3.2e-82;
Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MTPFGPASSLPQSGFLRLCLQGVKIQDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
Db      1  MTPFGPASSLPQSGFLRLCLQGVKIQDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60

Qy      61  PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQ 120
Db      61  PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQ 120

Qy      121  QMEELGNAPALQPTQGMPPAFAPAFQRRAGGVLVASHLQSFLEVSVYRHLAQP 175
Db      121  QMEELGNAPALQPTQGMPPAFAPAFQRRAGGVLVASHLQSFLEVSVYRHLAQP 175

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Search completed: December 27, 2004, 13:34:27
Job time : 297.5 secs

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OM protein - protein search, using sw model

Run on: December 27, 2004, 13:11:24 ; Search time 20 Seconds
(without alignments)
580.283 Million cell updates/sec

Title: 10032108-2EDIT
Perfect score: 901
Sequence: 1 MTPPLGASSLPQSFLLRCLE.....SHLQSFLEVSRYRLRLAQP 175

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
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2: /cgn2_6/prodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfilesei.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	901	100.0	175	1	US-08-010-099-72
2	901	100.0	175	1	US-08-448-716-72
3	901	100.0	175	3	US-09-304-186-72
4	901	100.0	175	4	US-09-754-532-72
5	898	99.7	175	1	US-08-010-099-74
6	898	99.7	175	1	US-08-448-716-74
7	898	99.7	175	3	US-09-304-186-74
8	898	99.7	175	4	US-09-754-532-74
9	895	99.3	175	1	US-08-010-099-67
10	895	99.3	175	1	US-08-010-099-69
11	895	99.3	175	1	US-08-010-099-70
12	895	99.3	175	1	US-08-010-099-71
13	895	99.3	175	1	US-08-010-099-73
14	895	99.3	175	1	US-08-010-099-75
15	895	99.3	175	1	US-08-448-716-67
16	895	99.3	175	1	US-08-448-716-69
17	895	99.3	175	1	US-08-448-716-70
18	895	99.3	175	1	US-08-448-716-71
19	895	99.3	175	1	US-08-448-716-73
20	895	99.3	175	1	US-08-448-716-75
21	895	99.3	175	3	US-09-304-186-67
22	895	99.3	175	3	US-09-304-186-69
23	895	99.3	175	3	US-09-304-186-70
24	895	99.3	175	3	US-09-304-186-71
25	895	99.3	175	3	US-09-304-186-73
26	895	99.3	175	3	US-09-304-186-75
27	895	99.3	175	4	US-09-754-532-67

28	895	99.3	175	4	US-09-754-532-69	Sequence 69, Appl
29	895	99.3	175	4	US-09-754-532-70	Sequence 70, Appl
30	895	99.3	175	4	US-09-754-532-71	Sequence 71, Appl
31	895	99.3	175	4	US-09-754-532-73	Sequence 73, Appl
32	895	99.3	175	4	US-09-754-532-75	Sequence 75, Appl
33	892	99.0	175	1	US-08-010-099-2	Sequence 2, Appl
34	892	99.0	175	1	US-08-167-721-1	Sequence 1, Appl
35	892	99.0	175	1	US-08-428-732-6	Sequence 6, Appl
36	892	99.0	175	1	US-08-448-716-2	Sequence 2, Appl
37	892	99.0	175	2	US-08-321-510-2	Sequence 2, Appl
38	892	99.0	175	2	US-08-879-760-2	Sequence 2, Appl
39	892	99.0	175	3	US-09-304-186-2	Sequence 2, Appl
40	892	99.0	175	4	US-09-230-733-1	Sequence 1, Appl
41	892	99.0	175	4	US-09-479-313B-15	Sequence 15, Appl
42	892	99.0	175	4	US-09-754-532-2	Sequence 2, Appl
43	892	99.0	175	5	PCT-US95-01729-2	Sequence 2, Appl
44	889	98.7	175	1	US-08-010-099-68	Sequence 68, Appl
45	889	98.7	175	1	US-08-010-099-76	Sequence 76, Appl

ALIGNMENTS

RESULT 1
US-08-010-099-72
; Sequence 72, Application US/08010099
; Patent No. 5581476
; GENERAL INFORMATION:
; APPLICANT: Oselund, Timothy
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen, Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/010,099
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-010-099-72

Query Match 100.0%; Score 901; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 8.7e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MTPPLGASSLPQSFLLRCLEQVRKIQDGAALQERLCATYRLCHPELVLLGHSIGPWA	60
DB	1	MTPPLGASSLPQSFLLRCLEQVRKIQDGAALQERLCATYRLCHPELVLLGHSIGPWA	60
QY	61	PLSSCPQALQAGCISQLHSLGFLYQGLQALEGISPELPTLDTLQLDVADFATTIQW	120
DB	61	PLSSCPQALQAGCISQLHSLGFLYQGLQALEGISPELPTLDTLQLDVADFATTIQW	120

QY 121 QMEELGMAPALPTQGGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRHLAQP 175
Db 121 QMEELGMAPALPTQGGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRHLAQP 175

RESULT 2

US-08-448-716-72
; Sequence 72, Application US/08448716
; Patent No. 5790421
; GENERAL INFORMATION:
; APPLICANT: Osslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,716
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-448-716-72

Query Match 100.0%; Score 901; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 8.7e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPGLPASSLPQSFLRLCLQEVKIQDGAALQERLCATYRLCHPEELVLLGHSIGIPWA 60
Db 1 MTPGLPASSLPQSFLRLCLQEVKIQDGAALQERLCATYRLCHPEELVLLGHSIGIPWA 60
QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTPLDTLQLDVADFATTIWQ 120
Db 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTPLDTLQLDVADFATTIWQ 120
QY 121 QMEELGMAPALPTQGGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRHLAQP 175
Db 121 QMEELGMAPALPTQGGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRHLAQP 175

RESULT 3

US-09-304-186-72
; Sequence 72, Application US/09304186
; Patent No. 6261550
; GENERAL INFORMATION:
; APPLICANT: Osslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California

; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/304,186
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-304-186-72

Query Match 100.0%; Score 901; DB 3; Length 175;
Best Local Similarity 100.0%; Pred. No. 8.7e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTPGLPASSLPQSFLRLCLQEVKIQDGAALQERLCATYRLCHPEELVLLGHSIGIPWA 60
Db 1 MTPGLPASSLPQSFLRLCLQEVKIQDGAALQERLCATYRLCHPEELVLLGHSIGIPWA 60
QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTPLDTLQLDVADFATTIWQ 120
Db 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTPLDTLQLDVADFATTIWQ 120
QY 121 QMEELGMAPALPTQGGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRHLAQP 175
Db 121 QMEELGMAPALPTQGGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRHLAQP 175

RESULT 4

US-09-754-532-72
; Sequence 72, Application US/09754532
; Patent No. 6632426
; GENERAL INFORMATION:
; APPLICANT: Osslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,532
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

NAME: Pessin, Karol
REGISTRATION NUMBER: 34,899
TELECOMMUNICATION INFORMATION:
TELEPHONE: 805/499-5725
TELEFAX: 805/499-8011
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-754-532-72

Query Match 100.0%; Score 901; DB 4; Length 175;
Best Local Similarity 100.0%; Pred. No. 8.7e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGASSLPQSFLRLCQLQVRRIOGDGAALQERLCATYRLCHPELVLLGHSGLGIPWA 60
DB 1 MTPLGASSLPQSFLRLCQLQVRRIOGDGAALQERLCATYRLCHPELVLLGHSGLGIPWA 60
QY 61 PLSSCPQALQAGCLSQLHSLGFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIQ 120
DB 61 PLSSCPQALQAGCLSQLHSLGFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIQ 120
QY 121 QMEELGMAPALQPTQGAMPAPASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGMAPALQPTQGAMPAPASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 5
US-08-010-099-74
Sequence 74, Application US/08010099
Patent No. 5581476
GENERAL INFORMATION:
APPLICANT: Osslund, Timothy D.
TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen, Inc.
STREET: Amgen Center, 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/010,099
FILING DATE: 24-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Pessin, Karol
REGISTRATION NUMBER: 34,899
TELECOMMUNICATION INFORMATION:
TELEPHONE: 805/499-5725
TELEFAX: 805/499-8011
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-448-716-74

Query Match 99.7%; Score 898; DB 1; Length 175;
Best Local Similarity 99.4%; Pred. No. 1.9e-91;
Matches 174; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGASSLPQSFLRLCQLQVRRIOGDGAALQERLCATYRLCHPELVLLGHSGLGIPWA 60
DB 1 MTPLGASSLPQSFLRLCQLQVRRIOGDGAALQERLCATYRLCHPELVLLGHSGLGIPWA 60
QY 61 PLSSCPQALQAGCLSQLHSLGFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIQ 120
DB 61 PLSSCPQALQAGCLSQLHSLGFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIQ 120
QY 121 QMEELGMAPALQPTQGAMPAPASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGMAPALQPTQGAMPAPASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 6
US-08-448-716-74
Sequence 74, Application US/08448716
Patent No. 5790421
GENERAL INFORMATION:
APPLICANT: Osslund, Timothy D.
TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen, Inc.
STREET: Amgen Center, 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: United States of America
ZIP: 91320-1789
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,716
FILING DATE: 24-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Pessin, Karol
REGISTRATION NUMBER: 34,899
TELECOMMUNICATION INFORMATION:
TELEPHONE: 805/499-5725
TELEFAX: 805/499-8011
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-448-716-74

Query Match 99.7%; Score 898; DB 1; Length 175;
Best Local Similarity 99.4%; Pred. No. 1.9e-91;
Matches 174; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGASSLPQSFLRLCQLQVRRIOGDGAALQERLCATYRLCHPELVLLGHSGLGIPWA 60
DB 1 MTPLGASSLPQSFLRLCQLQVRRIOGDGAALQERLCATYRLCHPELVLLGHSGLGIPWA 60
QY 61 PLSSCPQALQAGCLSQLHSLGFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIQ 120
DB 61 PLSSCPQALQAGCLSQLHSLGFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIQ 120
QY 121 QMEELGMAPALQPTQGAMPAPASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGMAPALQPTQGAMPAPASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 7
US-09-304-186-74
Sequence 74, Application US/09304186
Patent No. 6261550
GENERAL INFORMATION:
APPLICANT: Osslund, Timothy D.

;; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
;; NUMBER OF SEQUENCES: 110
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Amgen Inc.
;; STREET: Amgen Center, 1840 DeHavilland Drive
;; CITY: Thousand Oaks
;; STATE: California
;; COUNTRY: United States of America
;; ZIP: 91320-1789
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/304,186
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/448,716
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Pessin, Karol
;; REGISTRATION NUMBER: 34,899
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 805/499-5725
;; TELEFAX: 805/499-8011
;; INFORMATION FOR SEQ ID NO: 74:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 175 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-09-304-186-74

Query Match 99.7%; Score 898; DB 3; Length 175;
Best Local Similarity 99.4%; Pred. No. 1.9e-91;
Matches 174; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTPLGPAASSLPQSFLRLCLQVRRKIQDGAALQERLCATYRLCHPEELVLLGHSLGIPWA 60
DB 1 MTPLGPAASSLPQSFLRLCLQVRRKIQDGAALQERLCATYRLCHPEELVLLGHSLGIPWA 60
QY 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELPTLDTLQLDVADFATTIQQ 120
DB 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELPTLDTLQLDVADFATTIQQ 120
QY 121 QMEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 8
US-09-754-532-74
;; Sequence 74, Application US/09/754532
;; Patent No. 6632426
;; GENERAL INFORMATION:
;; APPLICANT: Oselund, Timothy D.
;; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
;; NUMBER OF SEQUENCES: 110
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Amgen Inc.
;; STREET: Amgen Center, 1840 DeHavilland Drive
;; CITY: Thousand Oaks
;; STATE: California
;; COUNTRY: United States of America
;; ZIP: 91320-1789
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/754,532
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/448,716
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Pessin, Karol
;; REGISTRATION NUMBER: 34,899
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 805/499-5725
;; TELEFAX: 805/499-8011
;; INFORMATION FOR SEQ ID NO: 74:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 175 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-09-754-532-74

Query Match 99.7%; Score 898; DB 4; Length 175;
Best Local Similarity 99.4%; Pred. No. 1.9e-91;
Matches 174; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTPLGPAASSLPQSFLRLCLQVRRKIQDGAALQERLCATYRLCHPEELVLLGHSLGIPWA 60
DB 1 MTPLGPAASSLPQSFLRLCLQVRRKIQDGAALQERLCATYRLCHPEELVLLGHSLGIPWA 60
QY 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELPTLDTLQLDVADFATTIQQ 120
DB 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELPTLDTLQLDVADFATTIQQ 120
QY 121 QMEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 9
US-08-010-099-67
;; Sequence 67, Application US/08010099
;; Patent No. 5581476
;; GENERAL INFORMATION:
;; APPLICANT: Oselund, Timothy
;; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
;; NUMBER OF SEQUENCES: 110
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Amgen, Inc.
;; STREET: Amgen Center, 1840 DeHavilland Drive
;; CITY: Thousand Oaks
;; STATE: California
;; COUNTRY: USA
;; ZIP: 91320-1789
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/010,099
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Pessin, Karol
;; REGISTRATION NUMBER: 34,899
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 805/499-5725
;; TELEFAX: 805/499-8011
;; INFORMATION FOR SEQ ID NO: 67:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 175 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein

US-08-010-099-67

Query Match 99.3%; Score 895; DB 1; Length 175;
Best Local Similarity 98.9%; Pred. No. 4e-91;
Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPGLPASSLPQSFLRLCLQVQRKIQDGAALQERLCATYRLCHPELVLLGHSGLGPWA 60
DB 1 MTPGLPASSLPQSFLRLCLQVQRKIQDGAALQERLCATYRLCHPELVLLGHSGLGPWA 60

QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPDLTDLQDVADFATTIQQ 120
DB 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPDLTDLQDVADFATTIQQ 120

QY 121 QMEELGNAPALQPTQGMPPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGNAPALQPTQGMPPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 10

US-08-010-099-69
; Sequence 69, Application US/08010099
; Patent No. 5581476
; GENERAL INFORMATION:
; APPLICANT: Osslund, Timothy
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen, Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/010,099
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-010-099-69

US-08-010-099-69

Query Match 99.3%; Score 895; DB 1; Length 175;
Best Local Similarity 98.9%; Pred. No. 4e-91;
Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPGLPASSLPQSFLRLCLQVQRKIQDGAALQERLCATYRLCHPELVLLGHSGLGPWA 60
DB 1 MTPGLPASSLPQSFLRLCLQVQRKIQDGAALQERLCATYRLCHPELVLLGHSGLGPWA 60

QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPDLTDLQDVADFATTIQQ 120
DB 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPDLTDLQDVADFATTIQQ 120

QY 121 QMEELGNAPALQPTQGMPPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGNAPALQPTQGMPPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 11

US-08-010-099-70
; Sequence 70, Application US/08010099
; Patent No. 5581476
; GENERAL INFORMATION:
; APPLICANT: Osslund, Timothy
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen, Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/010,099
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-010-099-70

Query Match 99.3%; Score 895; DB 1; Length 175;
Best Local Similarity 98.9%; Pred. No. 4e-91;
Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPGLPASSLPQSFLRLCLQVQRKIQDGAALQERLCATYRLCHPELVLLGHSGLGPWA 60
DB 1 MTPGLPASSLPQSFLRLCLQVQRKIQDGAALQERLCATYRLCHPELVLLGHSGLGPWA 60

QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPDLTDLQDVADFATTIQQ 120
DB 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPDLTDLQDVADFATTIQQ 120

QY 121 QMEELGNAPALQPTQGMPPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGNAPALQPTQGMPPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 12

US-08-010-099-71
; Sequence 71, Application US/08010099
; Patent No. 5581476
; GENERAL INFORMATION:
; APPLICANT: Osslund, Timothy
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen, Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk

```
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/010,099
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pessin, Karol
REGISTRATION NUMBER: 34,899
TELECOMMUNICATION INFORMATION:
TELEPHONE: 805/499-8011
TELEFAX: 805/499-8011
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-010-099-71

Query Match 99.3%; Score 895; DB 1; Length 175;
Best Local Similarity 98.9%; Pred. No. 4e-91;
Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPGPAASSLPQSFLRLCRLQVRIQGDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
DB 1 MTPGPAASSLPQSFLRLCRLQVRIQGDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
QY 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELPTLDTLQLDVADFATTIQQ 120
DB 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELPTLDTLQLDVADFATTIQQ 120
QY 121 QMEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 14
US-08-010-099-75
Sequence 75, Application US/08010099
Patent No. 5581476
GENERAL INFORMATION:
APPLICANT: Osslund, Timothy
TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen, Inc.
STREET: Amgen Center, 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/010,099
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pessin, Karol
REGISTRATION NUMBER: 34,899
TELECOMMUNICATION INFORMATION:
TELEPHONE: 805/499-5725
TELEFAX: 805/499-8011
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-010-099-75

Query Match 99.3%; Score 895; DB 1; Length 175;
Best Local Similarity 98.9%; Pred. No. 4e-91;
Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPGPAASSLPQSFLRLCRLQVRIQGDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
DB 1 MTPGPAASSLPQSFLRLCRLQVRIQGDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
QY 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELPTLDTLQLDVADFATTIQQ 120
DB 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELPTLDTLQLDVADFATTIQQ 120
QY 121 QMEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/010,099
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pessin, Karol
REGISTRATION NUMBER: 34,899
TELECOMMUNICATION INFORMATION:
TELEPHONE: 805/499-8011
TELEFAX: 805/499-8011
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-010-099-73

Query Match 99.3%; Score 895; DB 1; Length 175;
Best Local Similarity 98.9%; Pred. No. 4e-91;
Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPGPAASSLPQSFLRLCRLQVRIQGDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
DB 1 MTPGPAASSLPQSFLRLCRLQVRIQGDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
QY 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELPTLDTLQLDVADFATTIQQ 120
DB 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELPTLDTLQLDVADFATTIQQ 120
QY 121 QMEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 13
US-08-010-099-73
Sequence 73, Application US/08010099
Patent No. 5581476
GENERAL INFORMATION:
APPLICANT: Osslund, Timothy
TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen, Inc.
STREET: Amgen Center, 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/010,099
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pessin, Karol
REGISTRATION NUMBER: 34,899
TELECOMMUNICATION INFORMATION:
TELEPHONE: 805/499-5725
TELEFAX: 805/499-8011
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
TOPOLOGY: linear
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RESULT 15
US-08-448-716-67
; Sequence 67, Application US/08448716
; Patent No. 5790421
; GENERAL INFORMATION:
; APPLICANT: Oslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,716
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-448-716-67

Query Match 99.3%; Score 895; DB 1; Length 175;
Best Local Similarity 98.9%; Pred. No. 4e-91;
Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTPLGPASSLPQSFLRLCLQVQRKIQDGAALQERLCATYRLCHPEELVLLGHSIGIPWA 60
DB 1 MTPLGPASSLPQSFLRLCLQVQRKIQDGAALQERLCATYRLCHPEELVLLGHSIGIPWA 60
QY 61 PLSSCPQALQALAGCLSQLHSGFLYQGLLQALEGISPELGTPLDTLQLDVADFATTIWQ 120
DB 61 PLSSCPQALQALAGCLSQLHSGFLYQGLLQALEGISPELGTPLDTLQLDVADFATTIWQ 120
QY 121 QMEELGMALOPTQGMAPAFASAFORRAGGVLVASHLOSFLVSVYRLRHQAQP 175
DB 121 QMEELGMALOPTQGMAPAFASAFORRAGGVLVASHLOSFLVSVYRLRHQAQP 175

Search completed: December 27, 2004, 13:17:22
Job time : 21 secs

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GenCore version 5.1.6
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QM protein - protein search, using sw model

Run on: December 27, 2004, 13:11:24 ; Search time 63.5 Seconds
(without alignments)
1585.678 Million cell updates/sec

Title: 10032108-2

Perfect score: 901

Sequence: 1 MTPGLPASSLPQSLFKCLE.....SHLQSFLEVSRYVLRHLAQP 175

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374546 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	896	99.4	200	Q8N4W3	Q8N4W3 homo sapien
2	884.5	98.2	207	1 CSF3 HUMAN	P09919 homo.sapien
3	744	82.6	194	1 CSF3 FELCA	O02708 felis silve
4	744	82.6	195	2 Q9GJU0	O9GJU0 felis silve
5	739	82.0	175	1 CSF3 CANFA	P35834 canis famil
6	738	81.9	174	1 CSF3 SHEEP	O28746 ovis aries
7	727	80.7	195	1 CSF3 BOVIN	F35833 bos taurus
8	702	77.9	195	1 CSF3 PIG	O02837 sus scrofa
9	642	71.3	208	1 CSF3 MOUSE	P09920 mus musculus
10	635	70.5	214	2 P977I2	P977I2 rattus norv
11	511	56.7	127	2 Q8MKE0	Q8MKE0 equus cabal
12	304	33.7	201	1 MGP CHICK	F13854 gallus gall
13	111	12.3	241	2 Q90YI0	Q90YI0 gallus gall
14	110.5	12.3	212	2 Q8MJ75	Q8MJ75 sus scrofa
15	108	12.0	208	2 Q9XT80	Q9XT80 delphinapte
16	106.5	11.8	212	1 IL6 PIG	P26893 sus scrofa
17	101	11.2	205	1 IL6 ORCOR	O28747 orcinus orc
18	100	11.1	208	1 IL6 HORSE	Q95181 equus cabal
19	96	10.7	189	2 Q6NZ82	Q6NZ82 homo sapien
20	96	10.7	189	2 Q9H2A5	Q9H2A5 homo sapien
21	96	10.7	189	2 AAH66267	AAH66267 homo sapi
22	95	10.5	208	1 IL6 FELCA	P41683 felis silve
23	94.5	10.5	455	2 Q8D706	Q8D706 vibrio vuln
24	94	10.4	345	2 Q9KTL6	Q9KTL6 vibrio chol
25	93	10.3	189	2 Q9NPF7	Q9NPF7 homo sapien
26	93	10.3	189	2 AAH66268	AAH66268 homo sapi
27	93	10.3	189	2 AAQ89442	AAQ89442 homo sapi
28	93	10.3	189	2 AAH67511	AAH67511 homo sapi
29	93	10.3	189	2 AAH67512	AAH67512 homo sapi
30	93	10.3	189	2 AAH67513	AAH67513 homo sapi
31	91	10.1	189	2 Q6NZ80	Q6NZ80 homo sapien

32	89.5	10.1	189	2	AAH66269	AAH66269 homo sapi
33	89.5	9.9	214	2	Q8MKE5	Q8MKE5 sus scrofa
34	89.5	9.9	2175	1	HMCU DROME	P10180 drosophila
35	88.5	9.8	666	2	Q9A523	Q9A523 caulobacter
36	88.5	9.8	786	2	Q9I019	Q9I019 pseudomonas
37	88.5	9.8	1931	2	Q8RJY3	Q8RJY3 stigmatala
38	88	9.8	290	2	Q9P0S7	Q9P0S7 homo sapien
39	86	9.5	208	1	IL6 BOVIN	P26892 bos taurus
40	86	9.5	502	2	Q34008	Q34008 beta vulgar
41	86	9.5	788	2	Q8CF87	Q8CF87 mus musculu
42	86	9.5	850	2	Q7TQ21	Q7TQ21 mus musculu
43	86	9.5	851	2	Q8CF88	Q8CF88 mus musculu
44	86	9.5	852	2	Q811T9	Q811T9 mus musculu
45	85.5	9.5	211	2	Q865W7	Q865W7 camelus bac

ALIGNMENTS

RESULT 1

ID	Q8N4W3	PRELIMINARY;	PRT;	200 AA.
AC	Q8N4W3;			
DT	01-OCT-2002 (TrEMBLrel. 22, Created)			
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)			
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)			
DE	Colony stimulating factor 3, isoform c.			
GN	Name=CSF3;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Skin;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant L., Scheetz T.E.,			
RA	Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Skin;			
RA	Strausberg R.;			
RL	Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC033245; AAH3245.1; -			
DR	HSSP; P09919; 1GNC.			
DR	GO; GO:0005576; C:extracellular; IEA.			
DR	GO; GO:0005125; F:cytokine activity; IEA.			
DR	GO; GO:0005138; F:interleukin-6 receptor binding; IEA.			
DR	GO; GO:0006955; P:immune response; IEA.			
DR	InterPro; IPR009079; 4 helix cytokine.			
DR	InterPro; IPR003629; GCSF MGF.			
DR	InterPro; IPR003573; IL6 MGF GCSF.			
DR	InterPro; IPR003574; Interleukin_6.			
DR	Pfam; PF00489; IL6; 1.			
DR	PRINTS; PR00433; IL6GCSFMGF.			

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DR PRINTS; PR00434; INTERLEUKIN.
DR ProDom; PD008388; GCSF MGF; 1.
DR ProDom; PD004356; Interleukin_6; 1.
DR SWART; SW00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
SQ SEQUENCE 200 AA; 21543 MW; 8648AA5B329A96C CRC64;

Query Match          99.4%; Score 896; DB 2; Length 200;
Best Local Similarity 100.0%; Pred. No. 7.4e-74;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TPLGPASSLPQSFLKCLQVRIQSGAALQKLCATYKLCHEBELVLGHSLGIPWAP 61
DB 27 TPLGPASSLPQSFLKCLQVRIQSGAALQKLCATYKLCHEBELVLGHSLGIPWAP 86
OY 62 LSSCPQALQACLSQLHSLGLYQGLQALQSGISPELGPTLDTLQLDVADPATTIWOQ 121
DB 87 LSSCPQALQACLSQLHSLGLYQGLQALQSGISPELGPTLDTLQLDVADPATTIWOQ 146
OY 122 MEELGNAPALQPTQGAMPAPASAFQRRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 147 MEELGNAPALQPTQGAMPAPASAFQRRAGGVLVASHLQSFLEVSRYVLRHLAQP 200

RESULT 2
CSF3 HUMAN STANDARD; PRT; 207 AA.
AC P09919;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Granulocyte colony-stimulating factor precursor (G-CSF) (Pluripoiectin)
DE (Pilgrastim) (Lenograstim).
GN Name=CSF3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86118679; PubMed=3484805;
RA Nagata S., Teuchiya M., Asano S., Kaziro Y., Yamazaki T., Yamamoto O.,
RA Hirata Y., Kubota N., Oheda M., Nomura H., Ono M.;
RT "Molecular cloning and expression of cDNA for human granulocyte
RT colony-stimulating factor.";
RL Nature 319:415-418 (1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86220137; PubMed=2423327;
RA Nagata S., Teuchiya M., Asano S., Yamamoto O., Hirata Y., Kubota N.,
RA Oheda M., Nomura H., Yamazaki T.;
RT "The chromosomal gene structure and two mRNAs for human granulocyte
RT colony-stimulating factor.";
RL EMBO J. 5:575-581 (1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=87196936; PubMed=3494801;
RA Devlin J.J., Devlin P.E., Myambo K., Lilly M.B., Rado T.A.,
RA Warren M.K.;
RT "Expression of granulocyte colony-stimulating factor by human cell
RT lines.";
RL J. Leukoc. Biol. 41:302-306 (1987).
RN [4]
RP SEQUENCE FROM N.A., AND VARIANTS MET-157 AND THR-174.
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA Nickerson D.A.;
RT "SeattLeSNPs. NHLBI HL66682 program for genomic applications, UW-
RT FHCRS, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 19-207 FROM N.A.
RX MEDLINE=86151684; PubMed=2420009;
RA Souza L.M., Boone T.C., Gabrilove J., Lai P.H., Zsebo K.M.,
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RA Murdock D.C., Chazin V.R., Bruszewski J., Lu H., Chen K.K.,
RA Barendt J., Platzer E., Moore M.A.S., Mertelsmann R., Welte K.;
RT "Recombinant human granulocyte colony-stimulating factor: effects on
RT normal and leukemic myeloid cells.";
RL Science 232:61-66 (1986).
RN [6]
RP CARBOHYDRATE-LINKAGE SITE.
RX MEDLINE=93293942; PubMed=7685769;
RA Clogston C.L., Hu S., Boone T.C., Lu H.S.;
RT "Glycosidase digestion, electrophoresis and chromatographic analysis
RT of recombinant human granulocyte colony-stimulating factor glycoforms
RT produced in Chinese hamster ovary cells.";
RL J. Chromatogr. A 637:55-62 (1993).
RN [7]
RP STRUCTURE BY NMR.
RX MEDLINE=93106200; PubMed=1281794;
RA Zink T., Ross A., Ambrosius D., Rudolph R., Holak T.A.;
RT "Secondary structure of human granulocyte colony-stimulating factor
RT derived from NMR spectroscopy.";
RL FEBS Lett. 314:435-439 (1992).
RN [8]
RP STRUCTURE BY NMR.
RX MEDLINE=94304859; PubMed=7518249;
RA Zink T., Ross A., Luers K., Cieslar C., Rudolph R., Holak T.A.;
RT "Structure and dynamics of the human granulocyte colony-stimulating
RT factor determined by NMR spectroscopy. Loop mobility in a four-helix-
RT bundle protein.";
RL Biochemistry 33:8453-8463 (1994).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=93281718; PubMed=7685117;
RA Hill C.P., Osslund T.D., Eisenberg D.;
RT "The structure of granulocyte-colony-stimulating factor and its
RT relationship to other growth factors.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:5167-5171 (1993).
CC -!- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
CC cytokines that act in hematopoiesis by controlling the production,
CC differentiation, and function of 2 related white cell populations
CC of the blood, the granulocytes and the monocytes-macrophages. This
CC CSF induces granulocytes.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=P09919-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=P09919-2; Sequence=VSP 002673;
CC -!- PTM: O-glycan consists of Gal-GalNAc disaccharide which can be
CC modified with up to two sialic acid residues (done in
CC recombinantly expressed G-CSF from CHO cells).
CC -!- PHARMACEUTICAL: Available under the names Neupogen or Granulokine
CC (Amgen/Roche) and Granocyte (Rhône-Poulenc). Used to treat
CC neutropenia (a disorder characterized by an extremely low number
CC of neutrophils in blood).
CC -!- SIMILARITY: Belongs to the IL-6 superfamily.
CC -!- CAUTION: Ref.4 misquotes the gene name as "CSF1".
CC -!- DATABASE: NAME=Neupogen/Granulokine;
CC NOTE=Clinical information on Neupogen/Granulokine;
CC WWW="http://www.neupogen.com/";
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X03438; CAA27168.1; -
CC EMBL; M13008; AAA03056.1; -
CC EMBL; X03656; CAA27291.1; -
CC EMBL; X03655; CAA27290.1; -
CC DR
CC DR
CC DR
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DR EMBL; AF388025; AAK62469.1; -.
DR EMBL; M17706; AAA35882.1; -.
DR PIR; A24573; A24573.
DR PDB; 1CD9; X-ray; A/C=30-207.
DR PDB; 1GNC; NMR; Q=30-207.
DR PDB; 1PGR; X-ray; A/C/E/G=30-207.
DR PDB; 1RHG; X-ray; A/B/C=31-207.
DR Genew; HGNC:2438; CSF3.
DR MIM; 138970; -.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005130; F:granulocyte colony-stimulating factor recep. . .; TAS.
DR GO; GO:0007275; P:development; TAS.
DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
DR InterPro; IPR009079; 4 helix_cytokine.
DR InterPro; IPR003629; IL6_MGF_GCSF.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRODOM; PD008388; GCSF_MGF; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW 3D-structure; Alternative splicing; Cytokine; Glycoprotein;
KW Growth factor; Pharmaceutical; Polymorphism; Signal.
FT SIGNAL 1 30 Granulocyte colony-stimulating factor.
FT CHAIN 31 207
FT DISULFID 69 75
FT DISULFID 97 107
FT CARBOHYD 166 166
FT VARSPIC 66 68
FT VARIANT 157 157
FT VARIANT 174 174
FT HELIX 41 65
FT HELIX 69 71
FT HELIX 77 86
FT TURN 87 88
FT HELIX 105 124
FT TURN 125 127
FT TURN 130 132
FT HELIX 133 156
FT TURN 157 158
FT HELIX 176 203
FT TURN 204 204
SQ SEQUENCE 207 AA; 22293 MW; 421F635ECC776996 CRC64;
Query Match 98.2%; Score 884.5; DB 1; Length 207;
Best Local Similarity 98.3%; Pred. No. 8.7e-73;
Matches 174; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
QY 2 TPLGPASSLPQSFLKCLEQVRKIQGDGAALQEKLVSECATYKLCHEPELVLLGHSIGIP 58
DB 31 TPLGPASSLPQSFLKCLEQVRKIQGDGAALQEKLVSECATYKLCHEPELVLLGHSIGIP 90
QY 59 WAPLSSCPQALQAGCLSQLHSGFLYQGLLQALAGISPELGPTLDTLQDVADPATTI 118
DB 91 WAPLSSCPQALQAGCLSQLHSGFLYQGLLQALAGISPELGPTLDTLQDVADPATTI 150
QY 119 WQMEELGMAPALQPTQGMAMPASAFQRRAGGVLVASHLQSFLEVSRYVRLHAQP 175
DB 151 WQMEELGMAPALQPTQGMAMPASAFQRRAGGVLVASHLQSFLEVSRYVRLHAQP 207
RESULT 3
CSF3 FELCA STANDARD; PRT; 194 AA.
AC 002708;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Granulocyte colony-stimulating factor precursor (G-CSF) (Fragment).
```

```
GN Name=CSF3;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=European Shorthair; TISSUE=Lung;
RX MEDLINE=21389237; PubMed=11497496; DOI=10.1006/cyto.2001.0910;
RA Dunham S.P., Onions D.E.;
RT "Isolation, nucleotide sequence and expression of a cDNA encoding
RL Cytokine 14:347-351(2001).
CC -!- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
CC cytokines that act in hematopoiesis by controlling the production,
CC differentiation, and function of 2 related white cell populations
CC of the blood, the granulocytes and the monocytes-macrophages. This
CC CSF induces granulocytes (By similarity).
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: O-glycosylated (By similarity).
CC -!- SIMILARITY: Belongs to the IL-6 superfamily.
CC
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL; Y08558; CAA69853.1; -.
DR PIR; T09255; T09255.
DR HSSP; P09919; 1RHG.
DR InterPro; IPR009079; 4 helix_cytokine.
DR InterPro; IPR003629; GCSF_MGF.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRODOM; PD008388; GCSF_MGF; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT NON_TER 1 1
FT SIGNAL <1 20 Potential.
FT CHAIN 21 194 Granulocyte colony-stimulating factor.
FT DISULFID 56 62 By similarity.
FT DISULFID 84 94 By similarity.
FT CARBOHYD 153 153 O-linked (GlcNAc...) (By similarity).
SQ SEQUENCE 194 AA; 21154 MW; F72B7AB3DAE7385E CRC64;
Query Match 82.6%; Score 744; DB 1; Length 194;
Best Local Similarity 81.0%; Pred. No. 5.8e-60;
Matches 141; Conservative 11; Mismatches 22; Indels 0; Gaps 0;
QY 2 TPLGPASSLPQSFLKCLEQVRKIQGDGAALQEKLVSECATYKLCHEPELVLLGHSIGIPWAP 61
DB 21 TPLGPASSLPQSFLKCLEQVRKIQGDGAALQEKLVSECATYKLCHEPELVLLGHSIGIPWAP 80
QY 62 LSSCPQALQAGCLSQLHSGFLYQGLLQALAGISPELGPTLDTLQDVADPATTI 121
DB 81 LSSCPQALQAGCLSQLHSGFLYQGLLQALAGISPELGPTLDTLQDVADPATTI 140
QY 122 MEELGMAPALQPTQGMAMPASAFQRRAGGVLVASHLQSFLEVSRYVRLHAQP 175
DB 141 MEDVGNAPVPTQGTMTFTSAFQRRAGGVLVASHLQSFLEVSRYVRLHAQP 194
RESULT 4
Q9GUU0 PRELIMINARY; PRT; 195 AA.
ID Q9GUU0
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RN  SEQUENCE FROM N.A.
RP  MEDLINE=95102116; PubMed=7528579;
RA  O'Brien P.M., Seow H.F., Rothel J.S., Wood P.R.;
RT  "Cloning and sequencing of an ovine granulocyte colony-stimulating
RT  factor cDNA.";
RL  DNA Seq. 4:339-342(1994).
CC  -1- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
CC  cytokines that act in hematopoiesis by controlling the production,
CC  differentiation, and function of 2 related white cell populations
CC  of the blood, the granulocytes and the monocytes-macrophages. This
CC  CSF induces granulocytes (By similarity).
CC  -1- SUBUNIT: Monomer.
CC  -1- SUBCELLULAR LOCATION: Secreted.
CC  -1- PTM: O-glycosylated (By similarity).
CC  -1- SIMILARITY: Belongs to the IL-6 superfamily.
CC  -----
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; L07939; AAA68006.1; -.
DR  PIR; T10268; T10268.
DR  HSP; P09919; IRHG.
DR  InterPro; IPR009079; 4 helix cytokine.
DR  InterPro; IPR003629; GCSF MGF.
DR  InterPro; IPR003573; IL6_MGF_GCSF.
DR  Pfam; PF00489; IL6; 1.
DR  PRINTS; PR00433; IL6GCSFMGF.
DR  ProDom; PD008388; GCSF MGF; 1.
DR  SMART; SM00126; IL6; 1.
DR  ProSITE; PS00254; INTERLEUKIN_6; 1.
KW  Cytokine; Glycoprotein; Growth factor.
FT  DISULFID 36 42 By similarity.
FT  DISULFID 64 74 By similarity.
FT  CARBOHYD 133 133 O-linked (GalNAc...) (By similarity).
FT  SEQUENCE 174 AA; 18806 MW; BA5AA8P8D23ACDIE CRC64;

Query Match 81.9%; Score 738; DB 1; Length 174;
Best Local Similarity 82.2%; Pred. No. 1.8e-59;
Matches 143; Conservative 10; Mismatches 21; Indels 0; Gaps 0;

QY  2 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQKLCATYKLCHEPELVLLGHSIGIPWAP 61
Db  1 TPLGPARSUPQSFLKLCLEQVRKIQDGAELQERLCATHKLCHEPELVLLGHSIGIPQAP 60

QY  62 LSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELQPTLDTLQLDVADPATTIWOQ 121
Db  61 LSSCPSQSLLQTSCLQHLGFLYQGLLQALAGISPELAPTLDLTQLDVTDFATNIWLQ 120

QY  122 MEELGMAPALQPTQGMPPAFASFORRAGVLVASHLQSFLEVSRYVRLHLAQP 175
Db  121 MEDLGVAPAVQPTQGTMTFTSAFORRAGVLVASQLRPLGLAYRGLRYLAEP 174

RESULT 7
CSF3_BOVIN
ID  CSF3_BOVIN STANDARD; PRT; 195 AA.
AC  P35833; Q9TV89;
DT  01-JUN-1994 (Rel. 29, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DT  01-OCT-2004 (Rel. 45, Last annotation update)
DE  Granulocyte colony-stimulating factor precursor (G-CSF).
GN  Name=CSF3; Synonym=GCSF;
OS  Bos taurus (Bovine).
OC  Eukaryota; Chordata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC  Bovinae; Bos.
OC  NCBI_TaxID=9913;

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RN  SEQUENCE FROM N.A.
RP  STRAIN=Holstein;
RA  Heidari M., Kehrl M.B. Jr.;
RT  "Cloning, sequencing, and analysis of cDNA encoding bovine granulocyte
RT  colony stimulating factor.";
RL  Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
CC  [2]
RN  X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
RP  MEDLINE=94076341; PubMed=7504736;
RA  Lovejoy B., Cascio D., Eisenberg D.;
RT  "Crystal structure of canine and bovine granulocyte-colony stimulating
RT  factor (G-CSF).";
RL  J. Mol. Biol. 234:640-653(1993).
CC  -1- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
CC  cytokines that act in hematopoiesis by controlling the production,
CC  differentiation, and function of 2 related white cell populations
CC  of the blood, the granulocytes and the monocytes-macrophages. This
CC  CSF induces granulocytes.
CC  -1- SUBUNIT: Monomer.
CC  -1- SUBCELLULAR LOCATION: Secreted.
CC  -1- PTM: O-glycosylated.
CC  -1- SIMILARITY: Belongs to the IL-6 superfamily.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; AF092533; AAD16102.1; -.
DR  PDB; 1BGC; X-ray; @=22-195.
DR  InterPro; IPR009079; 4 helix cytokine.
DR  InterPro; IPR003629; GCSF MGF.
DR  InterPro; IPR003573; IL6_MGF_GCSF.
DR  Pfam; PF00489; IL6; 1.
DR  PRINTS; PR00433; IL6GCSFMGF.
DR  ProDom; PD008388; GCSF MGF; 1.
DR  SMART; SM00126; IL6; 1.
DR  ProSITE; PS00254; INTERLEUKIN_6; 1.
KW  3D-structure; Cytokine; Glycoprotein; Growth factor; Signal.
FT  SIGNAL 1 21 Potential.
FT  CHAIN 22 195 Granulocyte colony-stimulating factor.
FT  DISULFID 57 63
FT  DISULFID 85 95
FT  CARBOHYD 154 154
FT  CONFLICT 93 94 O-linked (GalNAc...) (By similarity).
FT  HELIX 32 60 TS -> RG (in Ref. 2).
FT  HELIX 65 69
FT  TURN 70 71
FT  HELIX 72 75
FT  TURN 76 76
FT  HELIX 83 85
FT  TURN 87 89
FT  HELIX 92 112
FT  TURN 113 115
FT  TURN 118 120
FT  HELIX 121 145
FT  HELIX 164 191
FT  TURN 192 192
SQ  SEQUENCE 195 AA; 21431 MW; 8C06119E4ADFBA73 CRC64;

Query Match 80.7%; Score 727; DB 1; Length 195;
Best Local Similarity 81.0%; Pred. No. 2.1e-58;
Matches 141; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

QY  2 TPLGPASSLPQSFLKLCLEQVRKIQDGAALQKLCATYKLCHEPELVLLGHSIGIPWAP 61
Db  22 TPLGPARSUPQSFLKLCLEQVRKIQDGAELQERLCATHKLCHEPELVLLGHSIGIPQAP 81

QY  62 LSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELQPTLDTLQLDVADPATTIWOQ 121

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Db 82 LSSCSQSLQTSCLNQLHGGFLVYQGLLQALAGISPELAPTLDLTLDQDVTDFATNIWLQ 141
 QY 122 MBELGNAPALQPTQGMAMPFAFAFORRAGGVLVASHQSLFVSVYRVLRLHQAOP 175
 Db 142 MEDLGAAPAVQPTQGMAMPFTSAFORRAGGVLVASQHLRFLEFLAYRGLRYLAEP 195

RESULT 8

CSF3_PIG STANDARD; PRT; 195 AA.
 AC 002837; 019180;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Granulocyte colony-stimulating factor precursor (G-CSF).
 GN Name=CSF3;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kulmburg P.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Gloster S.E.; Sandeman R.M.; Strom A.D.G.;
 RT "Cloning of a cDNA and gene encoding porcine granulocyte-colony
 stimulating factor.";
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
 cytokines that act in hematopoiesis by controlling the production,
 differentiation, and function of 2 related white cell populations
 of the blood, the granulocytes and the monocytes-macrophages. This
 CSF induces granulocytes (By similarity).
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: O-glycosylated (By similarity).
 CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
 CC
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 CC
 CC EMBL; Y10494; CAA71518.1; -;
 CC EMBL; U68482; AAB70701.1; -;
 CC EMBL; U68481; AAB70700.1; -;
 CC HSP; P09919; IRLH.
 CC InterPro; IPR009079; 4_helix_cytokine.
 CC InterPro; IPR003629; GCSF_MGF.
 CC InterPro; IPR003573; IL6_MGF_GCSF.
 CC Pfam; PF00489; IL6; 1.
 CC PRINTS; PR00433; IL6GCSFMGF.
 CC ProDom; PD008386; GCSF_MGF; 1.
 CC SMART; SM00126; IL6; 1.
 CC PROSITE; PS00254; INTERLEUKIN_6; 1.
 CC Cytokine; Glycoprotein; Growth factor; Signal.
 CC SIGNAL 1 21 Potential.
 CC CHAIN 1 21 Granulocyte colony-stimulating factor.
 CC FT DISULFID 57 63 By similarity.
 CC FT DISULFID 85 95 By similarity.
 CC FT CARBOHYD 154 154 O-linked (GalNAc...) (By similarity).
 CC FT CONFLICT 123 123 A -> R (in Ref. 1).
 CC SEQUENCE 195 AA; 21214 MW; 84787E20DB0AEALC CRC64;

Query_Match 77.9%; Score 702; DB 1; Length 195;
 Best Local Similarity 79.2%; Pred. No. 4.1e-56;

Matches 137; Conservative 11; Mismatches 25; Indels 0; Gaps 0;
 QY 3 PLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWAPL 62
 Db 23 PLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWAPL 82
 QY 63 SSCPSQALQALAGCSLQSHGSLFLYQGLLQALAGISPELAPTLDLTLDQDVTDFATNIQOM 122
 Db 83 SSCPSQALQALAGCSLQSHGSLFLYQGLLQALAGISPELAPTLDLTLDQDVTDFATNIQOM 142
 QY 123 EELGNAPALQPTQGMAMPFAFAFORRAGGVLVASHQSLFVSVYRVLRLHQAOP 175
 Db 143 EDLRMAPASLPTQGTVPFTSAFORRAGGVLVASHQSLFVSVYRVLRLHQAOP 195

RESULT 9

CSF3_MOUSE STANDARD; PRT; 208 AA.
 AC P09920;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Granulocyte colony-stimulating factor precursor (G-CSF).
 GN Name=Csfg3; Synonyms=Csfg;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=87017003; PubMed=3489940;
 RT "Isolation and characterization of the cDNA for murine granulocyte
 colony-stimulating factor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:7633-7637(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=87190474; PubMed=3494605;
 RT "The chromosomal gene structure for murine granulocyte colony-
 stimulating factor.";
 RL Eur. J. Biochem. 165:7-12(1987).
 RN [3]
 RP PARTIAL SEQUENCE.
 RA Simpson R.J.; Nice E.C.; Nicola N.A.;
 RT "Structural studies on the murine granulocyte colony-stimulating
 factor.";
 RL Biol. Chem. Hoppe-Seyler 368:1327-1331(1987).
 CC -1- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
 cytokines that act in hematopoiesis by controlling the production,
 differentiation, and function of 2 related white cell populations
 of the blood, the granulocytes and the monocytes-macrophages. This
 CSF induces granulocytes.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: O-glycosylated (By similarity).
 CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
 CC
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 CC
 CC EMBL; M13926; AAA37672.1; -;
 CC EMBL; X05402; CAA28986.1; -;
 CC PIR; A29536; A26496.
 CC HSP; P09919; IRLH.
 CC MGI; MGI:1339751; Csfg3.
 CC InterPro; IPR009079; 4_helix_cytokine.

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=89231616; PubMed=2785450;
 RX Leutz A., Damm K., Sterneck E., Kowenz E., Ness S., Frank R.,
 RA Gausepohl H., Pan Y.-C.E., Smart J., Hayman M., Graf T.;
 RT "Molecular cloning of the chicken myelomonocytic growth factor (cmGF)
 RT reveals relationship to interleukin 6 and granulocyte colony
 RT stimulating factor.";
 RL EMBO J. 8:175-181(1989).
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=92195319; PubMed=1549124;
 RA Sterneck E., Blatner C., Graf T., Leutz A.;
 RT "Structure of the chicken myelomonocytic growth factor gene and
 RT specific activation of its promoter in avian myelomonocytic cells by
 RT protein kinases.";
 RL Mol. Cell. Biol. 12:1728-1735(1992).
 CC -1- FUNCTION: Hematopoietic growth factor that stimulates the
 CC proliferation and colony formation of normal and transformed avian
 CC cells of the myeloid lineage.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
 CC -----
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 CC -----
 DR EMBL; M85034; AAA48694.1; -;
 DR EMBL; X14477; CAA32639.1; -;
 DR PIR; A42247; A42247.
 DR HSP; P09919; IRHG.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR003629; GCSE MGF.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR InterPro; IPR003574; Interleukin_6.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PRINTS; PR00434; INTERLEUKIN6.
 DR ProDom; PD008388; GCSE_MGF; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 DR Glycoprotein; Growth factor; Signal.
 KW SIGNAL
 FT CHAIN 1 23 Myelomonocytic growth factor.
 FT DISULFID 24 201 By similarity.
 FT DISULFID 61 67 By similarity.
 FT DISULFID 89 99 By similarity.
 FT CARBOHYD 123 123 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 137 137 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 201 AA; 22373 MW; 240A8DD21B424456 CRC64;
 Query Match 33.7%; Score 304; DB 1; Length 201;
 Best Local Similarity 40.6%; Pred. No. 1.1e-19;
 Matches 67; Conservative 28; Mismatches .68; Indels 2; Gaps 1;
 QY 12 QSFLLKLEQVRKIQQDGAALQEKLCATYKLGSLGIPWAPLSSCPQALQ 71
 DB 36 QLFHLKLETRKIRGVDAALQRAVCDTFCLEELQVQDPHLVQAPLDQCHKRGFQ 95
 QY 72 LAGCLSHQSLGLFLYQGLLQALEGISPELGTDLTLDLVADPATTWQMEELGHPAL 131
 DB 96 AEVCFQIRAGLHAYHSDGLAVLELLENHTTLVETLQLDANLSSNIQQQMEDLGLDVT 155
 QY 132 QPTQ--CAMPAFASAFORRAGGVLVASHLQSFLEVSRYVRLHQA 174
 DB 156 LPAEQRSPPTFGPFOQVGGFILANFQFLETAVALRHAR 200

RESULT 13
 Q90YIO PRELIMINARY; PRT; 241 AA.
 AC Q90YIO;
 DT 01-DEC-2001 (TREMELrel. 19, Created)
 DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
 DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
 DE Interleukin-6 precursor.
 GN Name=IL-6;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RN SEQUENCE FROM N.A.
 RA Schneider K., Kias R., Kaspers B., Staeheli P.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RN SEQUENCE FROM N.A.
 RA Kaiser P., Rothwell L., Galyov E.E., Barrow P.A., Burnside J.,
 RA Wigley P.;
 RT "Differential cytokine expression in avian cells in response to
 RT invasion by Salmonella typhimurium, Salmonella enteritidis and
 RT Salmonella gallinarum.";
 RL Microbiology 146:3217-3226(2000).
 RN [3]
 RN SEQUENCE FROM N.A.
 RA Kaiser P.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ309540; CAC40812.1; -;
 DR EMBL; AJ250838; CAC15566.2; -;
 DR HSP; P05231; 1ALU.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005125; P:cytokine activity; IEA.
 DR GO; GO:0005138; P:interleukin-6 receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR003629; GCSE MGF.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR InterPro; IPR003574; Interleukin_6.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PRINTS; PR00434; INTERLEUKIN6.
 DR ProDom; PD008388; GCSE_MGF; 1.
 DR ProDom; PD004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 KW Signal.
 FT SIGNAL 1 47 Potential.
 FT CHAIN 48 241 mature CHIL-6.
 SQ SEQUENCE 241 AA; 26790 MW; 657F8049F25BD2F8 CRC64;
 Query Match 12.3%; Score 111; DB 2; Length 241;
 Best Local Similarity 22.2%; Pred. No. 0.062;
 Matches 46; Conservative 35; Mismatches 74; Indels 52; Gaps 7;
 QY 4 LGPASSLP-----QSFLKLEQVRKIQQDGAALQEKLCATYKLGCH 44
 DB 41 LPAAAVPLPAAADSSGEVLEEGARRALLDCEPLARVLRDRAVLQDQCKFTVCE 100
 QY 45 PEELVLHSLGIPWAPLSSCPQALQLAG-----CLSHQSLGLFLYQGLLQALEGISPE 99
 DB 101 NSMEMLVNRNLPL-----KVTBEDGCLLAGFDEEKCLTKLSSGLFAFYLFQIFTFDS 156
 QY 100 LGFTLDTLDLVADPATTWQMEELGMAPAQPTQGAMPAPASAFORRAGGV----- 153
 DB 157 EKQNVESLCYSTKHLAATIRQWV-----INPDEVIP--DAAQKSLLANKSDKW 206
 QY 154 ---VASHL-----QSFLEVSRYVRLH 172
 DB 207 IEKLTWHLILRDTFSFMKTVRAVRYL 233

RESULT 14

Q8MJ75	PRELIMINARY;	PRT;	212 AA.
Q8MJ75;			
Q8MJ75;			
01-OCT-2002	(TREMBLrel. 22, Created)		
01-OCT-2002	(TREMBLrel. 22, Last sequence update)		
01-WAR-2004	(TREMBLrel. 26, Last annotation update)		
DE	IL-6.		
DE	Sus scrofa (Pig).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.		
NCBI_TaxID=9823;			
[1]			
SEQUENCE FROM N.A.			
Lee D., Yoo H., Choi I.;			
Submitted (JUN-2002)	to the EMBL/GenBank/DBJ databases.		
EMBL; AF518322; AAM74938.1; -.			
HSP; P05231; 1ALU.			
GO; GO:0005576; C:cytoplasmic; IEA.			
GO; GO:0005125; F:cytokine activity; IEA.			
GO; GO:0005138; P:interleukin-6 receptor binding; IEA.			
GO; GO:0006955; P:immune response; IEA.			
InterPro; IPR009079; 4 helix_cytokine.			
InterPro; IPR003573; IL6_MGF_GCSF.			
InterPro; IPR003574; Interleukin_6.			
Pfam; PF00489; IL6; 1.			
PRINTS; PR00433; IL6GCSFMGF.			
PRINTS; PR00434; INTERLEUKIN6.			
ProDom; PD004356; Interleukin_6; 1.			
SMART; SM00126; IL6; 1.			
PROSITE; PS00254; INTERLEUKIN_6; 1.			
SEQUENCE	212 AA; 23881 MW; IPF540E70308CFD77 CRG64;		

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 27, 2004, 13:11:24 ; Search time 63.5 Seconds
(without alignments)
988.624 Million cell updates/sec

Title: 10032108-2EDIT

Perfect score: 901

Sequence: 1 MTPGLPASSLPQSLFLRLCLE.....SHLQSFLEVSRYVRLHLAQP 175

Scoring table: BLASUM62

Gapop 10.0 , Gapext 0.5

Searched: 202273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_238sep04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	901	100.0	175	2	AAR56558 G-CSF ana
2	898	99.7	175	2	AAR56560 G-CSF ana
3	896	99.4	174	7	ADK41237 Human gra
4	896	99.4	348	5	ABG32031 Single ch
5	895	99.3	175	2	AAR56555 G-CSF ana
6	895	99.3	175	2	AAR56553 G-CSF ana
7	895	99.3	175	2	AAR56559 G-CSF ana
8	895	99.3	175	2	AAR56557 G-CSF ana
9	895	99.3	175	2	AAR56556 G-CSF ana
10	893	99.1	348	5	ABG32030 Single ch
11	892	99.0	175	1	AAP71030 Sequence
12	892	99.0	175	1	AAP70732 Sequence
13	892	99.0	175	1	AAP90107 Human gra
14	892	99.0	175	1	AAP90170 Human gra
15	892	99.0	175	1	AAP91070 Human gra
16	892	99.0	175	2	AAR56559 Platelet
17	892	99.0	175	2	AAR56553 Recombina
18	892	99.0	175	2	AAR56554 Pegylated
19	892	99.0	175	2	AAR56557 Human gra
20	892	99.0	175	3	AAY78936 Granulocy
21	892	99.0	175	3	AAB14851 Human gra
22	892	99.0	175	3	AAY97017 Mature gr
23	892	99.0	175	3	AAB23758 Human gra
24	892	99.0	175	4	AAG67563 Amino aci
25	892	99.0	175	4	AAG67502 Amino aci

26	892	99.0	175	4	AAR56558	Human hg-
27	892	99.0	175	4	AAR56558	Human G-C
28	892	99.0	175	4	AAR56558	Recombina
29	892	99.0	175	5	AAR56558	Branchied
30	892	99.0	175	6	AAR56558	Recombina
31	892	99.0	175	8	AAR56558	Recombina
32	892	99.0	175	2	AAR56558	Recombina
33	890	98.8	174	7	ADK41238	Human gra
34	890	98.8	174	7	ADK41238	Human gra
35	890	98.8	174	7	ADK41238	Human gra
36	890	98.8	348	5	ABG32029	Single ch
37	889	98.7	175	2	AAR56552	G-CSF ana
38	889	98.7	175	2	AAR56552	G-CSF ana
39	889	98.7	175	2	AAR56552	G-CSF ana
40	889	98.7	175	2	AAR56552	G-CSF ana
41	889	98.7	175	2	AAR56552	G-CSF ana
42	889	98.7	175	2	AAR56552	G-CSF ana
43	889	98.7	175	2	AAR56552	G-CSF ana
44	889	98.7	759	8	ADL16718	Human stu
45	889	98.7	783	2	AAR39473	Prepro-HS

ALIGNMENTS

RESULT 1
AAR56558
ID AAR56558 standard; protein; 175 AA.
XX
AC AAR56558;
XX
DT 25-MAR-2003 (revised)
DT 21-MAR-1995 (first entry)
XX
DE G-CSF analogue, K17,35,41>R17,35,41.
XX
KW Granulocyte colony stimulating factor; G-CSF; 3-D structure; mutagenic;
KW hydrophobic; hydrophilic; resistant; proteolysis; activity; antagonist.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "May be absent"
FT Misc-difference 17 /label= K17R
FT Misc-difference 35 /label= K35R
FT Misc-difference 41 /label= K41R
FT Misc-difference 41 /label= K41R
XX
WO9417185-A1.
PD 04-AUG-1994.
XX
XX 25-JAN-1994; 94WO-US000913.
XX 28-JAN-1993; 93US-00010099.
XX (AMGE-) AMGEN INC.
XX
XX Osslund TD;
XX WPI; 1994-264099/32.
XX
XX Granulocyte colony stimulating factor analogues - with altered,
XX biological activity, identified by analysis of three-dimensional
XX structure of native protein.
XX
XX Claim 21; Page 96; 206pp; English.
XX
XX The sequences given in AAR56553-96 represent analogues of granulocyte
XX colony stimulating factor (G-CSF). These analogues contain at least one

CC changed residue wrt. wild type G-CSF. G-CSF is modified by site-directed
CC mutagenesis of the single stranded DNA M13 phage or by mutagenic PCR. The
CC amino acids which were to be changed were determined by displaying the 3-
CC D structure of G-CSF on a computer. It is now possible to predict
CC accurately how changes in G-CSF structure will alter the characteristics
CC of the protein, particularly hydrophobic and hydrophilic areas can be
CC characterised. These new analogues have controllably altered properties,
CC eg. better resistance to proteolysis, higher or lower activity, including
CC no hematopoietic at all, ie. antagonists, longer shelf, easier
CC formulation etc. (Updated on 25-MAR-2003 to correct PI field.) (Updated
CC on 25-MAR-2003 to correct PI field.)
CC
CC
SQ Sequence 175 AA;

Granulocyte colony stimulating factor analogues - with altered, biological activity, identified by analysis of three-dimensional structure of native protein.

Claim 23; Page 98; 206pp; English.

The sequences given in AAR56553-56 represent analogues of granulocyte colony stimulating factor (G-CSF). These analogues contain at least one changed residue wrt. wild type G-CSF. G-CSF is modified by site-directed mutagenesis of the single stranded DNA M13 phage or by mutagenic PCR. The amino acids which were to be changed were determined by displaying the 3-D structure of G-CSF on a computer. It is now possible to predict accurately how changes in G-CSF structure will alter the characteristics of the protein, particularly hydrophobic and hydrophilic areas can be characterised. These new analogues have controllably altered properties, eg. better resistance to proteolysis, higher or lower activity, including not hematopoietic at all, ie. antagonists, longer shelf, easier formulation etc. (Updated on 25-MAR-2003 to correct FN field.) (Updated on 25-MAR-2003 to correct PI field.)

Sequence 175 AA;

PR 22-MAR-2002; 2002DK-00000447.
XX 08-MAY-2002; 2002DK-00000708.
XX (MAXY-) MAXYGEN HOLDINGS LTD.
XX Nissen TL, Andersen KV, Hansen CK, Mikkelsen JM, Schambye HT;
XX WPI; 2003-221717/21.
XX New polypeptide conjugate exhibiting granulocyte colony-stimulating
PT factor activity, useful for preventing or treating neutropenia or
PT leukaemia due to chemotherapy or radiation therapy, AIDS or other
PT immunodeficiency diseases.
XX
PS Claim 6; Page: 106pp; English.
XX
XX The invention relates to a novel polypeptide conjugate exhibiting
CC granulocyte colony-stimulating factor activity (G-CSF). The polypeptide
CC conjugate comprises: a polypeptide comprising at least one substitution
CC selected from the group of K16R/Q, K34R/Q, and K40R/Q, and at least one
CC substitution selected from the group of T105K and S159K relative to the
CC amino acid sequence of hG-CSF having a 174 residue amino acid sequence,
CC given in the specification, or in a corresponding position relative to an
CC amino acid sequence having at least 80 % sequence identity with the 174
CC residue amino acid sequence, where the conjugate has 2-6 polyethylene
CC glycol moieties with a molecular weight of 1000-10000 Da attached to
CC attachment groups of the polypeptide; or a polypeptide comprising an
CC amino acid sequence that differs in at least one amino acid residue from
CC the amino acid sequence of hG-CSF having the sequence of the 174 residue
CC amino acid sequence, and with at least one non-polypeptide moiety
CC attached to an attachment group of the polypeptide, where the conjugate
CC has an in vitro bioactivity in the range of 2-30% of the bioactivity of
CC non-conjugated hG-CSF as determined by the luciferase assay. The G-CSF
CC conjugate has immunostimulant, anti-HIV, virucide, antibacterial,
CC fungicide, and cytostatic activities. The polypeptide conjugate is useful
CC as a pharmaceutical, or for preparing a pharmaceutical composition for
CC treating an insufficient neutrophil level. The pharmaceutical composition
CC is also useful for preventing and/or treating neutropenia or leukaemia
CC due to chemotherapy or radiation therapy, or due to HIV or another viral
CC infection. The polypeptide conjugate may also be used for treating AIDS
CC or other immunodeficiency diseases, bacterial infections, acute myeloid
CC leukaemia, or for antifungal therapy, particularly for treating systemic
CC or invasive candidiasis. This sequence represents a mutant human G-CSF
CC protein of the invention. Note: This sequence is not shown in the
CC specification. It has been created from the wild-type human G-CSF protein
CC sequence ADK41219 and from information provided in the claims.
XX
XX Sequence 174 AA;
SQ

Query Match 99.4%; Score 896; DB 7; Length 174;
Best Local Similarity 100.0%; Pred. No. 9.3e-90;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TPLGPASSLPQSFLLRCLBQVRKIQDGAALQERLCATYRLCHPELVLLGSLGIPWAP 61
DB 1 TPLGPASSLPQSFLLRCLBQVRKIQDGAALQERLCATYRLCHPELVLLGSLGIPWAP 60
QY 62 LSSCPQALQAGCLSQLHSLFLYQGLAQLEGISPELGPTLDTLOLDVADPATTIWQO 121
DB 61 LSSCPQALQAGCLSQLHSLFLYQGLAQLEGISPELGPTLDTLOLDVADPATTIWQO 120
QY 122 MBEELGNAPALQPTQGANPASFARAGGVLVASHLQSFLEYSVRLRLHAQP 175
DB 121 MBEELGNAPALQPTQGANPASFARAGGVLVASHLQSFLEYSVRLRLHAQP 174

RESULT 4
ID ABG32031
XX ABG32031 standard; protein; 348 AA.
AC ABG32031;
XX
XX 15-NOV-2002 (first entry)
DT

XX Single chain G-CSF dimer polypeptide mutant, #3.
DE
XX
KW Single-chain multimeric polypeptide; polyethylene glycol; PEG;
KW granulocyte colony stimulating factor; G-CSF; human;
KW haematopoietic disorder; radiation therapy; chemotherapy;
KW bone marrow transplantation; acquired immunodeficiency syndrome; AIDS;
KW immunodeficiency disease; leukaemia; acute myeloid leukaemia; half-life;
KW clearance; immunogenicity; bioavailability; single chain G-CSF dimer;
KW antihuman immunodeficiency virus; HIV; haemostatic; mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH 1. .174
FT Region polypeptide encoded by either ABS52516 or ABS52519"
FT /note= "This region is copy 1 of the monomeric G-CSF
FT Misc-difference 16 polypeptide encoded by either ABS52516 or ABS52519"
FT /note= "Wild-type Lys substituted by Arg"
FT Misc-difference 34
FT /note= "Wild-type Lys substituted by Arg"
FT Misc-difference 40
FT /note= "Wild-type Lys substituted by Arg"
FT Region 175. .348
FT /note= "This region is copy 2 of the monomeric G-CSF
FT Misc-difference 190 polypeptide encoded by ABS52517"
FT /note= "Wild-type Lys substituted by Arg"
FT Misc-difference 208
FT /note= "Wild-type Lys substituted by Arg"
FT Misc-difference 214
FT /note= "Wild-type Lys substituted by Arg"
XX WO200236626-A1.
XX 10-MAY-2002.
XX 01-NOV-2001; 2001WO-DK000724.
XX 02-NOV-2000; 2000DK-00001647.
XX (MAXY-) MAXYGEN APS.
PA (MAXY-) MAXYGEN HOLDINGS LTD.
XX Nissen TL, Jensen AD;
XX WPI; 2002-618972/66.
XX
XX Single chain multimeric polypeptide conjugate for treating hematopoietic
PT disorders, has two units of monomeric polypeptides linked via peptide
PT bond/linker and polymer group bound to attachment group of polypeptide.
XX
PS Example 7; Page: 108pp; English.
XX
XX The invention discloses a single-chain multimeric polypeptide conjugate
CC comprising at least two units of a monomeric polypeptide linked via a
CC peptide bond or a peptide linker, where the monomeric polypeptide is
CC biologically active in its monomeric form and has at least one polymer
CC group covalently bound to an attachment group of the polypeptide e.g.
CC polyethylene glycol (PEG). The polypeptide is preferably a single-chain
CC multimeric granulocyte colony stimulating factor (G-CSF) polypeptide
CC comprising at least two G-CSF polypeptide monomers, linked via a peptide
CC bond or a peptide linker, where at least one of the monomers is a variant
CC of wild-type human G-CSF comprising at least one amino acid residue
CC modification. The monomeric and multimeric polypeptides are useful in
CC therapy and for manufacture of a medicament for treatment of general
CC haematopoietic disorders, including disorders arising from radiation
CC therapy, chemotherapy or bone marrow transplantations, acquired
CC immunodeficiency syndrome (AIDS) or other immunodeficiency diseases,
CC leukaemia and acute myeloid leukaemia. The conjugate has one or more
CC important properties as compared to the native polypeptide, including
CC increased functional in vivo half-life, increased serum half-life,

CC reduced clearance, reduced immunogenicity and/or increased
CC bioavailability. Consequently, medical treatment with a conjugate offers
CC advantages including longer duration between injections and fewer side
CC effects. The sequence presented is the single chain G-CSF dimer
CC polypeptide mutant, #3. Note: This sequence was not shown in the
CC specification but was created by the indexer from information given in
CC example 7
XX
XX Sequence 348 AA;

Query Match 99.4%; Score 896; DB 5; Length 348;
Best Local Similarity 100.0%; Pred. No. 2.3e-89;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TPLGPASSLPQSFLRLCQVRIQDGAALQERLCATYRLCHPELVLLGSLGIPWAP 61
DB 1 TPLGPASSLPQSFLRLCQVRIQDGAALQERLCATYRLCHPELVLLGSLGIPWAP 60
QY 62 LSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIWO 121
DB 61 LSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIWO 120
QY 122 MEELGMAPALOPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSYRVLRLHAQP 175
DB 121 MEELGMAPALOPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSYRVLRLHAQP 174

RESULT 5
AAR56555
ID AAR56555 standard; protein; 175 AA.
XX
AC AAR56555;
XX
DT 25-MAR-2003 (revised)
DT 21-MAR-1995 (first entry)
XX
DE G-CSF analogue, K35R.
XX
KW Granulocyte colony stimulating factor; G-CSF; 3-D structure; mutagenic;
KW hydrophobic; hydrophilic; resistant; proteolysis; activity; antagonist.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "May be absent"
FT Misc-difference 35 /label= K35R
FT
XX
XX WO9417185-A1.
XX
XX 04-AUG-1994.
XX
XX 25-JAN-1994; 94WO-US000913.
XX
XX 28-JAN-1993; 93US-00010099.
XX
XX (AMGE-) AMGEN INC.
XX
XX Oeslund TD;
XX
XX WPI; 1994-264099/32.
XX
XX Granulocyte colony stimulating factor analogues - with altered,
XX biological activity, identified by analysis of three-dimensional
XX structure of native protein.
XX
XX Claim 18; Page 94; 206pp; English.
XX
XX The sequences given in AAR56553-96 represent analogues of granulocyte
XX colony stimulating factor (G-CSF). These analogues contain at least one
XX changed residue wrt. wild type G-CSF. G-CSF is modified by site-directed
XX mutagenesis of the single stranded DNA M13 phage or by mutagenic PCR. The

CC amino acids which were to be changed were determined by displaying the 3-
D structure of G-CSF on a computer. It is now possible to predict
CC accurately how changes in G-CSF structure will alter the characteristics
CC of the protein, particularly hydrophobic and hydrophilic areas can be
CC characterised. These new analogues have controllably altered properties,
CC eg. better resistance to proteolysis, higher or lower activity, including
CC no hemotopoietic at all, ie. antagonists, longer shelf, easier
CC formulation etc. (Updated on 25-MAR-2003 to correct PN field.) (Updated
XX on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 175 AA;

Query Match 99.3%; Score 895; DB 2; Length 175;
Best Local Similarity 98.9%; Pred. No. 1.2e-89;
Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGPASSLPQSFLRLCQVRIQDGAALQERLCATYRLCHPELVLLGSLGIPWA 60
DB 1 MTPLGPASSLPQSFLRLCQVRIQDGAALQERLCATYRLCHPELVLLGSLGIPWA 60
QY 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIWO 120
DB 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIWO 120
QY 121 QMEELGMAPALOPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSYRVLRLHAQP 175
DB 121 QMEELGMAPALOPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSYRVLRLHAQP 175

RESULT 6
AAR56553
ID AAR56553 standard; protein; 175 AA.
XX
AC AAR56553;
XX
DT 25-MAR-2003 (revised)
DT 21-MAR-1995 (first entry)
XX
DE G-CSF analogue, K17R.
XX
KW Granulocyte colony stimulating factor; G-CSF; 3-D structure; mutagenic;
KW hydrophobic; hydrophilic; resistant; proteolysis; activity; antagonist.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "May be absent"
FT Misc-difference 17 /label= K17R
FT
XX
XX WO9417185-A1.
XX
XX 04-AUG-1994.
XX
XX 25-JAN-1994; 94WO-US000913.
XX
XX 28-JAN-1993; 93US-00010099.
XX
XX (AMGE-) AMGEN INC.
XX
XX Oeslund TD;
XX
XX WPI; 1994-264099/32.
XX
XX Granulocyte colony stimulating factor analogues - with altered,
XX biological activity, identified by analysis of three-dimensional
XX structure of native protein.
XX
XX Claim 17; Page 92; 206pp; English.
XX
XX The sequences given in AAR56553-96 represent analogues of granulocyte
XX colony stimulating factor (G-CSF). These analogues contain at least one

CC changed residue wrt. wild type G-CSF. G-CSF is modified by site-directed
 CC mutagenesis of the single stranded DNA M13 phage or by mutagenic PCR. The
 CC amino acids which were to be changed were determined by displaying the 3-
 CC D structure of G-CSF on a computer. It is now possible to predict
 CC accurately how changes in G-CSF structure will alter the characteristics
 CC of the protein, particularly hydrophobic and hydrophilic areas can be
 CC characterised. These new analogues have controllably altered properties,
 CC eg. better resistance to proteolysis, higher or lower activity, including
 CC no hemagglutinating at all, ie. antagonists, longer shelf, easier
 CC formulation etc. (Updated on 25-MAR-2003 to correct PN field.) (Updated
 CC on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 175 AA;

Query Match 99.3%; Score 895; DB 2; Length 175;
 Best Local Similarity 98.9%; Pred. No. 1.2e-89;
 Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPGPAASSLPQSFLRLCLQEVKIQDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
 DB 1 MTPGPAASSLPQSFLRLCLQEVKIQDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
 QY 61 PLSSCPQALQAGLSQLHSGFLYQGLLQALEGSPGLPTLDTLQDVADPATTIQQ 120
 DB 61 PLSSCPQALQAGLSQLHSGFLYQGLLQALEGSPGLPTLDTLQDVADPATTIQQ 120
 QY 121 QMEELGNAPALQPTQAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 175
 DB 121 QMEELGNAPALQPTQAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 175

RESULT 7

AAR56559
 ID AAR56559 standard; protein; 175 AA.

XX AAR56559;

XX 25-MAR-2003 (revised)

DT 21-MAR-1995 (first entry)

XX G-CSF analogue, K24,35,41>R24,35,41.

XX Granulocyte colony stimulating factor; G-CSF; 3-D structure; mutagenic;
 KW hydrophobic; hydrophilic; resistant; proteolysis; activity; antagonist.
 XX Synthetic.

XX Key Location/Qualifiers
 FT Misc-difference 1 /note= "May be absent"
 FT Misc-difference 24 /label= K24R
 FT Misc-difference 35 /label= K35R
 FT Misc-difference 41 /label= K41R

XX WO9417185-A1.

XX 04-AUG-1994.

XX 25-JAN-1994; 94WO-US0000913.

XX 28-JAN-1993; 93US-00010099.

XX (AMGE-) AMGEN INC.

XX Ooslund TD;

XX WPI; 1994-264099/32.

XX Granulocyte colony stimulating factor analogues - with altered,
 PT biological activity, identified by analysis of three-dimensional

PT structure of native protein.

XX Claim 22; Page 97; 206pp; English.

XX The sequences given in AAR56553-96 represent analogues of granulocyte
 CC colony stimulating factor (G-CSF). These analogues contain at least one
 CC changed residue wrt. wild type G-CSF. G-CSF is modified by site-directed
 CC mutagenesis of the single stranded DNA M13 phage or by mutagenic PCR. The
 CC amino acids which were to be changed were determined by displaying the 3-
 CC D structure of G-CSF on a computer. It is now possible to predict
 CC accurately how changes in G-CSF structure will alter the characteristics
 CC of the protein, particularly hydrophobic and hydrophilic areas can be
 CC characterised. These new analogues have controllably altered properties,
 CC eg. better resistance to proteolysis, higher or lower activity, including
 CC no hemagglutinating at all, ie. antagonists, longer shelf, easier
 CC formulation etc. (Updated on 25-MAR-2003 to correct PN field.) (Updated
 CC on 25-MAR-2003 to correct PI field.)
 XX

SQ Sequence 175 AA;

Query Match 99.3%; Score 895; DB 2; Length 175;
 Best Local Similarity 98.9%; Pred. No. 1.2e-89;
 Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPGPAASSLPQSFLRLCLQEVKIQDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
 DB 1 MTPGPAASSLPQSFLRLCLQEVKIQDGAALQERLCATYRLCHPELVLLGHSIGIPWA 60
 QY 61 PLSSCPQALQAGLSQLHSGFLYQGLLQALEGSPGLPTLDTLQDVADPATTIQQ 120
 DB 61 PLSSCPQALQAGLSQLHSGFLYQGLLQALEGSPGLPTLDTLQDVADPATTIQQ 120
 QY 121 QMEELGNAPALQPTQAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 175
 DB 121 QMEELGNAPALQPTQAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 175

RESULT 8

AAR56557

ID AAR56557 standard; protein; 175 AA.

XX AAR56557;

XX 25-MAR-2003 (revised)

DT 21-MAR-1995 (first entry)

XX G-CSF analogue, K17,24,35>R17,24,35.

XX Granulocyte colony stimulating factor; G-CSF; 3-D structure; mutagenic;
 KW hydrophobic; hydrophilic; resistant; proteolysis; activity; antagonist.
 XX Synthetic.

XX Key Location/Qualifiers
 FT Misc-difference 1 /note= "May be absent"
 FT Misc-difference 17 /label= K17R
 FT Misc-difference 24 /label= K24R
 FT Misc-difference 35 /label= K35R

XX WO9417185-A1.

XX 04-AUG-1994.

XX 25-JAN-1994; 94WO-US0000913.

XX 28-JAN-1993; 93US-00010099.

XX (AMGE-) AMGEN INC.

XX

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PI Osslund TD;
XX WPI; 1994-264099/32.
XX
XX Granulocyte colony stimulating factor analogues - with altered,
XX PT biological activity, identified by analysis of three-dimensional
XX PT structure of native protein.
XX
XX Claim 20; Page 95-96; 206pp; English.
XX
XX The sequences given in AAR56553-96 represent analogues of granulocyte
XX CC colony stimulating factor (G-CSF). These analogues contain at least one
XX CC changed residue wrt. wild type G-CSF. G-CSF is modified by site-directed
XX CC mutagenesis of the single stranded DNA M13 phage or by mutagenic PCR. The
XX CC amino acids which were to be changed were determined by displaying the 3-
XX CC D structure of G-CSF on a computer. It is now possible to predict
XX CC accurately how changes in G-CSF structure will alter the characteristics
XX CC of the protein, particularly hydrophobic and hydrophilic areas can be
XX CC characterised. These new analogues have controllably altered properties,
XX CC eg. better resistance to proteolysis, higher or lower activity, including
XX CC no hematopoietic at all, ie. antagonists, longer shelf, easier
XX CC formulation etc. (Updated on 25-MAR-2003 to correct PN field.) (Updated
XX CC on 25-MAR-2003 to correct PI field.)
XX
XX Sequence 175 AA;
XX
Query Match 99.3%; Score 895; DB 2; Length 175;
Best Local Similarity 98.9%; Pred. No. 1.2e-89;
Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTPLGPASSLPQSFLRLCLLEQVRKIQDGAALQERLCATYRLCHPELVLLGHSLGIPWA 60
DB 1 MTPLGPASSLPQSFLRLCLLEQVRKIQDGAALQERLCATYRLCHPELVLLGHSLGIPWA 60
QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTPLDTLQLDVADFATTIQQ 120
DB 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTPLDTLQLDVADFATTIQQ 120
QY 121 QMEELGNAPALOPTQGNMPAFASAFQRRAGGVLVASHLQSFLEVSRYRVLHQAQP 175
DB 121 QMEELGNAPALOPTQGNMPAFASAFQRRAGGVLVASHLQSFLEVSRYRVLHQAQP 175

RESULT 9
AAR56556
ID AAR56556 standard; protein; 175 AA.
XX
XX AAR56556;
XX
XX 25-MAR-2003 (revised)
XX DT 21-MAR-1995 (first entry)
XX
XX G-CSF analogue, K41R.
XX
XX Granulocyte colony stimulating factor; G-CSF; 3-D structure; mutagenic;
XX KW hydrophobic; hydrophilic; resistant; proteolysis; activity; antagonist.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 1 /note= "May be absent"
XX FT Misc-difference 41 /label= K41R
XX
XX WO9417185-A1.
XX
XX 04-AUG-1994.
XX
XX 25-JAN-1994; 94WO-US0000913.
XX
XX 28-JAN-1993; 93US-00010099.
XX

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PA (AMGE-) AMGEN INC.
XX
XX Osslund TD;
XX
XX WPI; 1994-264099/32.
XX
XX Granulocyte colony stimulating factor analogues - with altered,
XX PT biological activity, identified by analysis of three-dimensional
XX PT structure of native protein.
XX
XX Claim 19; Page 94-95; 206pp; English.
XX
XX The sequences given in AAR56553-96 represent analogues of granulocyte
XX CC colony stimulating factor (G-CSF). These analogues contain at least one
XX CC changed residue wrt. wild type G-CSF. G-CSF is modified by site-directed
XX CC mutagenesis of the single stranded DNA M13 phage or by mutagenic PCR. The
XX CC amino acids which were to be changed were determined by displaying the 3-
XX CC D structure of G-CSF on a computer. It is now possible to predict
XX CC accurately how changes in G-CSF structure will alter the characteristics
XX CC of the protein, particularly hydrophobic and hydrophilic areas can be
XX CC characterised. These new analogues have controllably altered properties,
XX CC eg. better resistance to proteolysis, higher or lower activity, including
XX CC no hematopoietic at all, ie. antagonists, longer shelf, easier
XX CC formulation etc. (Updated on 25-MAR-2003 to correct PN field.) (Updated
XX CC on 25-MAR-2003 to correct PI field.)
XX
XX Sequence 175 AA;
XX
Query Match 99.3%; Score 895; DB 2; Length 175;
Best Local Similarity 98.9%; Pred. No. 1.2e-89;
Matches 173; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTPLGPASSLPQSFLRLCLLEQVRKIQDGAALQERLCATYRLCHPELVLLGHSLGIPWA 60
DB 1 MTPLGPASSLPQSFLRLCLLEQVRKIQDGAALQERLCATYRLCHPELVLLGHSLGIPWA 60
QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTPLDTLQLDVADFATTIQQ 120
DB 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTPLDTLQLDVADFATTIQQ 120
QY 121 QMEELGNAPALOPTQGNMPAFASAFQRRAGGVLVASHLQSFLEVSRYRVLHQAQP 175
DB 121 QMEELGNAPALOPTQGNMPAFASAFQRRAGGVLVASHLQSFLEVSRYRVLHQAQP 175

RESULT 10
ABG32030
ID ABG32030 standard; protein; 348 AA.
XX
XX ABG32030;
XX
XX 15-NOV-2002 (first entry)
XX
XX Single chain G-CSF dimer polypeptide mutant, #2.
XX
XX Single-chain multimeric polypeptide; polyethylene glycol; PEG;
XX KW granulocyte colony stimulating factor; G-CSF; human;
XX KW haematopoietic disorder; radiation therapy; chemotherapy;
XX KW bone marrow transplantation; acquired immunodeficiency syndrome; AIDS;
XX KW immunodeficiency disease; leukaemia; acute myeloid leukaemia; half-life;
XX KW clearance; immunogenicity; bioavailability; single chain G-CSF dimer;
XX KW antihuman immunodeficiency virus; HIV; haemostatic; mutant; mutein.
XX
XX Homo sapiens.
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX FT Region 1..174
XX FT /note= "This region is copy 1 of the monomeric G-CSF
XX FT polypeptide encoded by either ABS52516 or ABS52519"
XX FT Misc-difference 16
XX FT /note= "Wild-type Lys substituted by Arg"
XX FT Misc-difference 34

```

FT /note= "wild-type Lys substituted by Arg"
 FT 175. .348
 FT /note= "This region is copy 2 of the monomeric G-CSF
 FT polypeptide encoded by ABS52517"
 FT Misc-difference 130
 FT /note= "wild-type Lys substituted by Arg"
 FT Misc-difference 208
 FT /note= "wild-type Lys substituted by Arg"
 XX WO200236626-A1.
 XX 10-MAY-2002.
 XX 01-NOV-2001; 2001WO-DK000724.
 XX 02-NOV-2000; 2000DK-00001647.
 XX (MAXY-) MAXYGEN APS.
 XX (MAXY-) MAXYGEN HOLDINGS LTD.
 XX Nissen TL, Jensen AD;
 XX WPI; 2002-618972/66.
 XX Single chain multimeric polypeptide conjugate for treating hematopoietic
 XX disorders, has two units of monomeric polypeptides linked via peptide
 XX bond/linker and polymer group bound to attachment group of polypeptide.
 XX Example 7; Page; 108pp; English.
 XX The invention discloses a single-chain multimeric polypeptide conjugate
 XX comprising at least two units of a monomeric polypeptide linked via a
 XX peptide bond or a peptide linker, where the monomeric polypeptide is
 XX biologically active in its monomeric form and has at least one polymer
 XX group covalently bound to an attachment group of the polypeptide e.g.
 XX polyethylene glycol (PEG). The polypeptide is preferably a single-chain
 XX multimeric granulocyte colony stimulating factor (G-CSF) polypeptide
 XX comprising at least two G-CSF polypeptide monomers, linked via a peptide
 XX bond or a peptide linker, where at least one of the monomers is a variant
 XX of wild-type human G-CSF comprising at least one amino acid residue
 XX modification. The monomeric and multimeric polypeptides are useful in
 XX therapy and for manufacture of a medicament for treatment of general
 XX haematopoietic disorders, including disorders arising from radiation
 XX therapy, chemotherapy or bone marrow transplantations, acquired
 XX immunodeficiency syndrome (AIDS) or other immunodeficiency diseases,
 XX leukopenia and acute myeloid leukaemia. The conjugate has one or more
 XX important properties as compared to the native polypeptide, including
 XX increased functional in vivo half-life, increased serum half-life,
 XX reduced clearance, reduced immunogenicity and/or increased
 XX bioavailability. Consequently, medical treatment with a conjugate offers
 XX advantages including longer duration between injections and fewer side
 XX effects. The sequence presented is the single chain G-CSF dimer
 XX polypeptide mutant, #2. Note: This sequence was not shown in the
 XX specification but was created by the indexer from information given in
 XX example 7
 XX Sequence 348 AA;
 Query Match 99.1%; Score 893; DB 5; Length 348;
 Best Local Similarity 99.4%; Pred. No. 5e-89;
 Matches 173; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 TPLGPASSLPQSFLRLCQLVQKIQDGAALQERLCATYRLCHPELVLLGHSGLGPWP 61
 Db 1 TPLGPASSLPQSFLRLCQLVQKIQDGAALQERLCATYRLCHPELVLLGHSGLGPWP 60
 QY 62 LSSCPQALQAGCLSQLHSGFLYQGLLQALGEGISPELGTDLTLDLVADPATTIWQ 121
 Db 61 LSSCPQALQAGCLSQLHSGFLYQGLLQALGEGISPELGTDLTLDLVADPATTIWQ 120
 QY 122 MEELGNAPALOPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
 Db 121 MEELGNAPALOPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 174

RESULT 11
 AAP71030
 ID AAP71030 standard; protein; 175 AA.
 XX
 AC AAP71030;
 XX
 DT 29-MAY-1991 (first entry)
 XX
 DE Sequence of human granulocyte colony stimulating factor (hGCSF) type II.
 XX
 KW Myelogenous leukaemia therapy; neutrophil.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1
 FT /note= "optional"
 XX
 PN EP231819-A.
 XX
 PD 12-AUG-1987.
 XX
 PF 21-JAN-1987; 87EP-00100809.
 XX
 PR 22-JAN-1986; 86JP-00010281.
 XX
 PR 21-JAN-1987; 87JP-00010038.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 PI Tamura M, Hattori K;
 XX
 DR WPI; 1987-222837/32.
 XX
 PT Agent for treating myelogenous leukaemia - contains human granulocyte
 PT colony stimulating factor.
 XX
 PS Claim 3; Page 7; 7pp; English.
 XX
 CC hGCSF is the effective ingredient of an agent for the treatment of
 CC myelogenous leukaemia. The agent is used for increasing the no. of
 CC peripheral mature neutrophils in patients with myelogenous leukaemia and
 CC also prolonging life. Doses are 0.1-500, pref. 5-100 meg, 1-7 times/week.
 CC Type II hGCSF may be prepd. as in EP 8601138.7
 XX
 SQ Sequence 175 AA;
 Query Match 99.0%; Score 892; DB 1; Length 175;
 Best Local Similarity 98.3%; Pred. No. 2.6e-89;
 Matches 172; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTPLGPASSLPQSFLRLCQLVQKIQDGAALQERLCATYRLCHPELVLLGHSGLGPWA 60
 Db 1 MTPLGPASSLPQSFLRLCQLVQKIQDGAALQERLCATYRLCHPELVLLGHSGLGPWA 60
 QY 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALGEGISPELGTDLTLDLVADPATTIWQ 120
 Db 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALGEGISPELGTDLTLDLVADPATTIWQ 120
 QY 121 QMEELGNAPALOPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
 Db 121 QMEELGNAPALOPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
 RESULT 12
 AAP70732
 ID AAP70732 standard; protein; 175 AA.
 XX
 AC AAP70732;
 XX
 DT 25-MAR-2003 (revised)
 DT 26-APR-1991 (first entry)

XX DE Sequence encoded by human granulocyte colony stimulating factor (hpg-CSF)
 DE cDNA with an amino terminal methionine.
 XX KW Haematopoietic disorders; therapy; aplastic anaemia;
 KW bone marrow transplant; burn wounds; leukaemia.
 XX OS Homo sapiens.
 XX PN W08701132-A.
 XX PD 26-FEB-1987.
 XX PF 22-AUG-1986; 86WO-US001708.
 XX PR 23-AUG-1985; 85US-00768954.
 XX PR 23-AUG-1985; 85US-00768959.
 XX PR 03-MAR-1986; 86US-00835548.
 XX PA (KIRI) KIRIN AMGEN INC.
 XX PA (KIRI) KIRIN AMGEN INC.
 XX PA (AMGE-) AMGEN.
 XX PI Souza LM;
 XX DR WPI; 1987-064855/09.
 XX DR N-PSDB; AAN71091.
 XX PT Poly:peptide with granulocyte colony stimulating factor activity - obt'd.
 XX PT by recombinant DNA procedures for treating haematopoietic disorders.
 XX PS Example; pp42-43; 79pp; English.
 XX CC The examples describe procedures for the designing of probes for hpg-CSF
 CC cDNA and genomic clones, both of which are claimed. Specifically claimed
 CC are DNA sequences coding for (Ala 1)hpg-CSF; (Ser 36,42,64 and 74)hpg-CSF
 CC and the corresp. Met-1 cpds. The novelty is that hpg-CSF is the prod. of
 CC procaryotic or eucaryotic expression of an exogenous DNA sequence. The
 CC construction of hpg-CSF vectors is also described in the examples.
 CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to
 CC correct PA field.)
 XX SQ Sequence 175 AA;
 Query Match 99.0%; Score 892; DB 1; Length 175;
 Best Local Similarity 98.3%; Pred. No. 2.6e-89;
 Matches 172; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTPLGPASSLPOSFLRLCIEQVRKIQGDGAALQERLCATYRLCHPEELVLLGHSIGIPWA 60
 DB 1 MTPLGPASSLPOSFLRLCIEQVRKIQGDGAALQERLCATYRLCHPEELVLLGHSIGIPWA 60
 QY 61 FLSSCPSQALQAGCLSQLHSGLFLYQGLLQALEGISPELGTDLTLDVADPATTIQQ 120
 DB 61 FLSSCPSQALQAGCLSQLHSGLFLYQGLLQALEGISPELGTDLTLDVADPATTIQQ 120
 QY 121 QMEELGMAPALQTOGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYRLHQAQP 175
 DB 121 QMEELGMAPALQTOGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYRLHQAQP 175
 RESULT 13
 AAP90107
 ID AAP90107 standard; protein; 175 AA.
 XX AC AAP90107;
 XX AC AAP90107;
 XX DT 25-MAR-2003 (revised)
 XX DT 27-NOV-1989 (first entry)
 XX DE Human granulocyte colony stimulating factor.
 XX KW Human granulocyte colony stimulating factor; restriction sites;
 XX KW bone marrow precursor cells.
 XX OS Homo sapiens.
 XX PN GB2213821-A.
 XX PD 23-AUG-1989.
 XX PF 23-DEC-1987; 87GB-00030055.
 XX PR 23-DEC-1987; 87GB-00030055.
 XX PR 23-DEC-1987; 87GB-00030055.
 XX PA (BRBI-) BRIT BIO-TECHN LTD.
 XX KW Human granulocyte colony stimulating factor; restriction sites;

XX KW bone marrow precursor cells.
 XX OS Homo sapiens.
 XX PN GB2213821-A.
 XX PD 23-AUG-1989.
 XX PF 23-DEC-1987; 87GB-00030055.
 XX PR 23-DEC-1987; 87GB-00030055.
 XX PR 23-DEC-1987; 87GB-00030055.
 XX PA (BRBI-) BRIT BIO-TECHN LTD.
 XX PI Edwards RM;
 XX DR WPI; 1989-243775/34.
 XX PT Synthetic granulocyte colony stimulating factor gene - incorporating
 PT restriction sites for facilitating cassette mutagenesis and expression.
 XX PS Disclosure; Fig 3a; 24pp; English.
 XX CC G-CSF stimulates proliferation of specific bone marrow precursor cells
 CC and their differentiation into granulocytes. See also AAN90533. (Updated
 CC on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct
 CC PA field.)
 XX SQ Sequence 175 AA;
 Query Match 99.0%; Score 892; DB 1; Length 175;
 Best Local Similarity 98.3%; Pred. No. 2.6e-89;
 Matches 172; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTPLGPASSLPOSFLRLCIEQVRKIQGDGAALQERLCATYRLCHPEELVLLGHSIGIPWA 60
 DB 1 MTPLGPASSLPOSFLRLCIEQVRKIQGDGAALQERLCATYRLCHPEELVLLGHSIGIPWA 60
 QY 61 FLSSCPSQALQAGCLSQLHSGLFLYQGLLQALEGISPELGTDLTLDVADPATTIQQ 120
 DB 61 FLSSCPSQALQAGCLSQLHSGLFLYQGLLQALEGISPELGTDLTLDVADPATTIQQ 120
 QY 121 QMEELGMAPALQTOGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYRLHQAQP 175
 DB 121 QMEELGMAPALQTOGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYRLHQAQP 175
 RESULT 14
 AAP90170
 ID AAP90170 standard; protein; 175 AA.
 XX AC AAP90170;
 XX AC AAP90170;
 XX DT 25-MAR-2003 (revised)
 XX DT 27-NOV-1989 (first entry)
 XX DE Human granulocyte colony stimulating factor.
 XX KW Human granulocyte colony stimulating factor; restriction sites;
 XX KW bone marrow precursor cells.
 XX OS Homo sapiens.
 XX PN GB2213821-A.
 XX PD 23-AUG-1989.
 XX PF 23-DEC-1987; 87GB-00030055.
 XX PR 23-DEC-1987; 87GB-00030055.
 XX PR 23-DEC-1987; 87GB-00030055.
 XX PA (BRBI-) BRIT BIO-TECHN LTD.
 XX KW Human granulocyte colony stimulating factor; restriction sites;

PI Edwards RM;
XX DR WPI; 1989-243775/34.
XX
XX Synthetic granulocyte colony stimulating factor gene - incorporating
PT restriction sites for facilitating cassette mutagenesis and expression.
XX
XX Disclosure; Fig 3a; 24pp; English.
XX
XX G-CSF stimulates proliferation of specific bone marrow precursor cells
CC and their differentiation into granulocytes. See also AAN90533. (Updated
CC on 25-MAR-2003 to correct PA field.)
XX
XX Sequence 175 AA;
SQ

Query Match 99.0%; Score 892; DB 1; Length 175;
Best Local Similarity 98.3%; Pred. No. 2.6e-89;
Matches 172; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
1 MTPLGPASSLPQSFLRLCLQEQVRKIQGDGAALQERLCATYRICHPELVLLGHSLGIPWA 60
1 MTPLGPASSLPQSFLRLCLQEQVRKIQGDGAALQERLCATYRICHPELVLLGHSLGIPWA 60
61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTQLQDVADFATTIWQ 120
61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTQLQDVADFATTIWQ 120
121 QMEELGMAPALQPTQGMPPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
121 QMEELGMAPALQPTQGMPPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

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Job time : 64.5 secs

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Db 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTQLQDVADFATTIWQ 120
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Db 121 QMEELGMAPALQPTQGMPPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 15
AAP91070
ID AAP91070 standard; protein; 175 AA.
XX
AC AAP91070;
XX
DT 25-MAR-2003 (revised)
DT 27-NOV-1989 (first entry)
XX
DE Human granulocyte colony stimulating factor.
XX
KW Human granulocyte colony stimulating factor; restriction sites;
KW bone marrow precursor cells.
XX
OS Homo sapiens.
XX
PN GB2213821-A.
XX
PD 23-AUG-1989.
XX
PF 23-DEC-1987; 87GB-00030055.
XX
PR 23-DEC-1987; 87GB-00030055.
XX
XX (BRBI-) BRIT BIO-TECHN LTD.
XX
PI Edwards RM;
XX
XX WPI; 1989-243775/34.
XX
XX Synthetic granulocyte colony stimulating factor gene - incorporating
PT restriction sites for facilitating cassette mutagenesis and expression.
XX
XX Disclosure; Fig 3a; 24pp; English.
XX
XX G-CSF stimulates proliferation of specific bone marrow precursor cells
CC and their differentiation into granulocytes. See also AAN90533. (Updated
CC on 25-MAR-2003 to correct PA field.)
XX
XX Sequence 175 AA;
SQ

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OM protein - protein search, using sw model

Run on: December 27, 2004, 13:11:24 ; Search time 20 Seconds
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Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
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Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/prodata/1/iaa/backfilese1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	901	100.0	175	1	US-08-010-099-2
2	901	100.0	175	1	US-08-167-721-1
3	901	100.0	175	1	US-08-428-732-6
4	901	100.0	175	1	US-08-448-716-2
5	901	100.0	175	2	US-08-321-510-2
6	901	100.0	175	2	US-08-879-760-2
7	901	100.0	175	3	US-09-304-186-2
8	901	100.0	175	4	US-09-230-733-1
9	901	100.0	175	4	US-09-479-313B-15
10	901	100.0	175	4	US-09-754-532-2
11	901	100.0	175	5	PCT-US95-01729-2
12	898	99.7	175	1	US-08-010-099-67
13	898	99.7	175	1	US-08-010-099-68
14	898	99.7	175	1	US-08-010-099-69
15	898	99.7	175	1	US-08-010-099-70
16	898	99.7	175	1	US-08-010-099-76
17	898	99.7	175	1	US-08-010-099-92
18	898	99.7	175	1	US-08-010-099-93
19	898	99.7	175	1	US-08-010-099-99
20	898	99.7	175	1	US-08-448-716-67
21	898	99.7	175	1	US-08-448-716-68
22	898	99.7	175	1	US-08-448-716-69
23	898	99.7	175	1	US-08-448-716-70
24	898	99.7	175	1	US-08-448-716-76
25	898	99.7	175	1	US-08-448-716-92
26	898	99.7	175	1	US-08-448-716-93
27	898	99.7	175	1	US-08-448-716-99

28	898	99.7	175	3	US-09-304-186-67	Sequence 67, Appl
29	898	99.7	175	3	US-09-304-186-68	Sequence 68, Appl
30	898	99.7	175	3	US-09-304-186-69	Sequence 69, Appl
31	898	99.7	175	3	US-09-304-186-70	Sequence 70, Appl
32	898	99.7	175	3	US-09-304-186-76	Sequence 76, Appl
33	898	99.7	175	3	US-09-304-186-92	Sequence 92, Appl
34	898	99.7	175	3	US-09-304-186-93	Sequence 93, Appl
35	898	99.7	175	3	US-09-304-186-99	Sequence 99, Appl
36	898	99.7	175	4	US-09-754-532-67	Sequence 67, Appl
37	898	99.7	175	4	US-09-754-532-68	Sequence 68, Appl
38	898	99.7	175	4	US-09-754-532-69	Sequence 69, Appl
39	898	99.7	175	4	US-09-754-532-70	Sequence 70, Appl
40	898	99.7	175	4	US-09-754-532-76	Sequence 76, Appl
41	898	99.7	175	4	US-09-754-532-92	Sequence 92, Appl
42	898	99.7	175	4	US-09-754-532-93	Sequence 93, Appl
43	898	99.7	175	4	US-09-754-532-99	Sequence 99, Appl
44	898	99.7	175	5	PCT-US95-01752-2	Sequence 2, Appl
45	898	99.7	177	2	US-08-797-689-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-08-010-099-2
; Sequence 2, Application US/08010099
; Patent No. 5581476
; GENERAL INFORMATION:
; APPLICANT: Oselund, Timothy
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen, Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/010,099
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-010-099-2

Query Match 100.0%; Score 901; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.9e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MTPPLGPASSLPQSLKLEQVRKIQGDGAALQEKLCATYKLCHPPELVLLGSLIPWA	60
Db	1	MTPPLGPASSLPQSLKLEQVRKIQGDGAALQEKLCATYKLCHPPELVLLGSLIPWA	60
Qy	61	PLSSCPQALQAGCISQLHSGFLYQGLQALEGISPELPTDLTQLDQVADPATTIQ	120
Db	61	PLSSCPQALQAGCISQLHSGFLYQGLQALEGISPELPTDLTQLDQVADPATTIQ	120

QY 121 QMEELGMAPALOPTQGAMPAFASAFQRRAGGVVASHLQSFLEVSRYVLRHLAQP 175
Db |||||
121 QMEELGMAPALOPTQGAMPAFASAFQRRAGGVVASHLQSFLEVSRYVLRHLAQP 175

RESULT 2

US-08-167-721-1
; Sequence 1, Application US/08167721
; Patent No. 5597562
; GENERAL INFORMATION:
; APPLICANT: No. 5597562ura, Hideaki
; APPLICANT: Maruyama, Kazutoshi
; TITLE OF INVENTION: Oral Dosage Form of Biologically Active
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/167,721
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/994,076
; FILING DATE:
; APPLICATION NUMBER: US/07/709,622
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25447
; REFERENCE/DOCKET NUMBER: 11009/30403
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-167-721-1

Query Match 100.0%; Score 901; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.9e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTPGLPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGHSIGIPWA 60
Db |||||
1 MTPGLPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGHSIGIPWA 60
QY 61 PLSSCPQALQAGCISLHSGFLYQGLLQALEGISPELGTPLDTLQLDVADPATTIWQ 120
Db |||||
61 PLSSCPQALQAGCISLHSGFLYQGLLQALEGISPELGTPLDTLQLDVADPATTIWQ 120
QY 121 QMEELGMAPALOPTQGAMPAFASAFQRRAGGVVASHLQSFLEVSRYVLRHLAQP 175
Db |||||
121 QMEELGMAPALOPTQGAMPAFASAFQRRAGGVVASHLQSFLEVSRYVLRHLAQP 175

RESULT 3

US-08-428-732-6

; Sequence 6, Application US/08428732
; Patent No. 5606024
; GENERAL INFORMATION:
; APPLICANT: Boone, Thomas C.
; APPLICANT: Miller, Allan L.
; TITLE OF INVENTION: DNA Encoding Canine Granulocyte Colony
; TITLE OF INVENTION: Stimulating Factor (G-CSF)
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/428,732
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Crandall, Craig A.
; REFERENCE/DOCKET NUMBER: A-173-C2
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-428-732-6

Query Match 100.0%; Score 901; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.9e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTPGLPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGHSIGIPWA 60
Db |||||
1 MTPGLPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGHSIGIPWA 60
QY 61 PLSSCPQALQAGCISLHSGFLYQGLLQALEGISPELGTPLDTLQLDVADPATTIWQ 120
Db |||||
61 PLSSCPQALQAGCISLHSGFLYQGLLQALEGISPELGTPLDTLQLDVADPATTIWQ 120
QY 121 QMEELGMAPALOPTQGAMPAFASAFQRRAGGVVASHLQSFLEVSRYVLRHLAQP 175
Db |||||
121 QMEELGMAPALOPTQGAMPAFASAFQRRAGGVVASHLQSFLEVSRYVLRHLAQP 175

RESULT 4

US-08-448-716-2
; Sequence 2, Application US/08448716
; Patent No. 5790421
; GENERAL INFORMATION:
; APPLICANT: Osslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25

```

;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,716
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-448-716-2

Query Match      100.0%; Score 901; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.9e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGHSGLIPWA 60
DB 1 MTPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGHSGLIPWA 60
QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPPTLDTLQLDVADFATTIWQ 120
DB 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPPTLDTLQLDVADFATTIWQ 120
QY 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 175
DB 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 175

RESULT 5
US-08-321-510-2
; Sequence 2, Application US/08321510
; Patent No. 5824784
; GENERAL INFORMATION:
; APPLICANT: Kinstler, Olaf B.
; APPLICANT: Gabriel, Nancy E.
; APPLICANT: Farrar, Christine E.
; APPLICANT: DePrince, Randolph B.
; TITLE OF INVENTION: N-Terminally Chemically Modified Protein
; TITLE OF INVENTION: Composition and Methods
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/321,510
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol M.
; REFERENCE/DOCKET NUMBER: A-286
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-321-510-2

Query Match      100.0%; Score 901; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.9e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGHSGLIPWA 60
DB 1 MTPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGHSGLIPWA 60
QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPPTLDTLQLDVADFATTIWQ 120
DB 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPPTLDTLQLDVADFATTIWQ 120
QY 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 175
DB 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 175

RESULT 6
US-08-879-760-2
; Sequence 2, Application US/08879760
; Patent No. 5985265
; GENERAL INFORMATION:
; APPLICANT: Kinstler, Olaf B.
; APPLICANT: Gabriel, Nancy E.
; APPLICANT: Farrar, Christine E.
; APPLICANT: DePrince, Randolph B.
; TITLE OF INVENTION: N-Terminally Chemically Modified Protein
; TITLE OF INVENTION: Composition and Methods
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/321,510
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol M.
; REFERENCE/DOCKET NUMBER: A-286
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-879-760-2

Query Match      100.0%; Score 901; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.9e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGHSGLIPWA 60
DB 1 MTPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGHSGLIPWA 60
QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPPTLDTLQLDVADFATTIWQ 120
DB 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPPTLDTLQLDVADFATTIWQ 120
QY 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 175
DB 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 175
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QY 121 QMEELGMALPQTOGAMPAPAFASAFORRAGGVVASHLQSFLEVSVYRHLAQP 175
Db 121 QMEELGMALPQTOGAMPAPAFASAFORRAGGVVASHLQSFLEVSVYRHLAQP 175

RESULT 7

US-09-304-186-2
; Sequence 2, Application US/09304186
; Patent No. 6261550
; GENERAL INFORMATION:
; APPLICANT: Oselund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/304,186
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-304-186-2

Query Match 100.0%; Score 901; DB 3; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.9e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIPWA 60
Db 1 MTPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIPWA 60
QY 61 PLSSCPQALQAGLSQLHSGFLYQGLQALEGISPELPTLDTLQLDVADFATTIWQ 120
Db 61 PLSSCPQALQAGLSQLHSGFLYQGLQALEGISPELPTLDTLQLDVADFATTIWQ 120
QY 121 QMEELGMALPQTOGAMPAPAFASAFORRAGGVVASHLQSFLEVSVYRHLAQP 175
Db 121 QMEELGMALPQTOGAMPAPAFASAFORRAGGVVASHLQSFLEVSVYRHLAQP 175

RESULT 8

US-09-230-733-1
; Sequence 1, Application US/09230733
; Patent No. 6583267
; GENERAL INFORMATION:
; APPLICANT: Yamasaki, Motoo
; APPLICANT: Suzawa, Toshiyuki
; APPLICANT: Kobayashi, Ken
; APPLICANT: Konishi, No. 6583267oru

; APPLICANT: Akinaga, Shiro
; APPLICANT: Matuyama, Kumiko
; TITLE OF INVENTION: CHEMICALLY MODIFIED POLYPEPTIDES
; FILE REFERENCE: 249-102
; CURRENT APPLICATION NUMBER: US/09/230,733
; CURRENT FILING DATE: 1999-02-03
; EARLIER APPLICATION NUMBER: PCT/JP98/02504
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: JP 9-149342
; EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: polypeptide
; OTHER INFORMATION: having hG-CSF activity
US-09-230-733-1

Query Match 100.0%; Score 901; DB 4; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.9e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIPWA 60
Db 1 MTPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIPWA 60
QY 61 PLSSCPQALQAGLSQLHSGFLYQGLQALEGISPELPTLDTLQLDVADFATTIWQ 120
Db 61 PLSSCPQALQAGLSQLHSGFLYQGLQALEGISPELPTLDTLQLDVADFATTIWQ 120
QY 121 QMEELGMALPQTOGAMPAPAFASAFORRAGGVVASHLQSFLEVSVYRHLAQP 175
Db 121 QMEELGMALPQTOGAMPAPAFASAFORRAGGVVASHLQSFLEVSVYRHLAQP 175

RESULT 9

US-09-479-313B-15
; Sequence 15, Application US/09479313B
; Patent No. 6627186
; GENERAL INFORMATION:
; APPLICANT: Dahiyat, Bassil I.
; APPLICANT: Luo, Peizhi
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEIN VARIANTS OF hG-CSF WITH GRANULOPOIETIC
; FILE OF INVENTION: ACTIVITY
; FILE REFERENCE: A-67614-2/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/479,313B
; CURRENT FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: US 60/115,131
; PRIOR FILING DATE: 1999-01-06
; PRIOR APPLICATION NUMBER: US 60/118,831
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 15
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (2)..()
US-09-479-313B-15

Query Match 100.0%; Score 901; DB 4; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.9e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIPWA 60
Db 1 MTPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIPWA 60

QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALLEGISPELGPTLDTLQLDVADPATTIQQ 120
DB 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALLEGISPELGPTLDTLQLDVADPATTIQQ 120
QY 121 QMEELGNAPALQPTQGMAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHQAQP 175
DB 121 QMEELGNAPALQPTQGMAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHQAQP 175

RESULT 10

US-09-754-532-2
; Sequence 2, Application US/09754532
; Patent No. 6632426
; GENERAL INFORMATION:
; APPLICANT: Oeslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,532
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-01729-2

Query Match 100.0%; Score 901; DB 4; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.9e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTPLGPASSLPQSFLKLCLEQVRKIQGDGAALQEKLCATYKLCPELVLLGHSLGIPWA 60
DB 1 MTPLGPASSLPQSFLKLCLEQVRKIQGDGAALQEKLCATYKLCPELVLLGHSLGIPWA 60
QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALLEGISPELGPTLDTLQLDVADPATTIQQ 120
DB 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALLEGISPELGPTLDTLQLDVADPATTIQQ 120
QY 121 QMEELGNAPALQPTQGMAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHQAQP 175
DB 121 QMEELGNAPALQPTQGMAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHQAQP 175

US-09-754-532-2
Query Match 100.0%; Score 901; DB 4; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.9e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTPLGPASSLPQSFLKLCLEQVRKIQGDGAALQEKLCATYKLCPELVLLGHSLGIPWA 60
DB 1 MTPLGPASSLPQSFLKLCLEQVRKIQGDGAALQEKLCATYKLCPELVLLGHSLGIPWA 60
QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALLEGISPELGPTLDTLQLDVADPATTIQQ 120
DB 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALLEGISPELGPTLDTLQLDVADPATTIQQ 120
QY 121 QMEELGNAPALQPTQGMAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHQAQP 175
DB 121 QMEELGNAPALQPTQGMAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHQAQP 175

RESULT 11

PCT-US95-01729-2
; Sequence 2, Application PC/TUS9501729
; GENERAL INFORMATION:
; APPLICANT: AMGEN INC.
; TITLE OF INVENTION: N-Terminally Chemically Modified Protein

; TITLE OF INVENTION: Composition and Methods
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01729
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol M.
; REFERENCE/DOCKET NUMBER: A-286
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-01729-2

Query Match 100.0%; Score 901; DB 5; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.9e-92;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGPASSLPQSFLKLCLEQVRKIQGDGAALQEKLCATYKLCPELVLLGHSLGIPWA 60
DB 1 MTPLGPASSLPQSFLKLCLEQVRKIQGDGAALQEKLCATYKLCPELVLLGHSLGIPWA 60
QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALLEGISPELGPTLDTLQLDVADPATTIQQ 120
DB 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALLEGISPELGPTLDTLQLDVADPATTIQQ 120
QY 121 QMEELGNAPALQPTQGMAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHQAQP 175
DB 121 QMEELGNAPALQPTQGMAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHQAQP 175

RESULT 12

US-08-010-099-67
; Sequence 67, Application US/08010099
; Patent No. 5581476
; GENERAL INFORMATION:
; APPLICANT: Oeslund, Timothy
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen, Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/010,099
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol

; NUMBER OF SEQUENCES: 110
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Amgen, Inc.
 ; STREET: Amgen Center, 1840 DeHavilland Drive
 ; CITY: Thousand Oaks
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 91320-1789
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/010,099
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Pessin, Karol
 ; REGISTRATION NUMBER: 34,899
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 805/499-5725
 ; TELEFAX: 805/499-8011
 ; INFORMATION FOR SEQ ID NO: 70:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 175 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-010-099-70

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Search completed: December 27, 2004, 13:17:21
 Job time : 22 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2004, 13:14:34 ; Search time 297.5 Seconds
(without alignments)
211.245 Million cell updates/sec

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Perfect score: 901
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Gapop 10.0 , Gapext 0.5

Searched: 1595201 seqs, 359116952 residues

Total number of hits satisfying chosen parameters: 1595201

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	901	100.0	175	9	US-09-921-114-2
4	901	100.0	175	11	US-09-817-725-2
5	901	100.0	175	14	US-10-131-956-2
6	901	100.0	175	14	US-10-264-846-2
7	901	100.0	175	14	US-10-009-792A-21
8	901	100.0	175	14	US-10-032-108-2
9	901	100.0	175	14	US-10-345-639A-2
10	901	100.0	175	14	US-10-365-418-1
11	901	100.0	175	14	US-10-436-784-2
12	901	100.0	175	14	US-10-168-956A-3
13	901	100.0	175	15	US-10-632-695-15

14	901	100.0	175	16	US-10-659-295-38	Sequence 38, Appl
15	901	100.0	175	16	US-10-750-797-2	Sequence 2, Appl
16	901	100.0	175	17	US-10-751-242-2	Sequence 2, Appl
17	898	99.7	175	9	US-09-754-532-67	Sequence 67, Appl
18	898	99.7	175	9	US-09-754-532-68	Sequence 68, Appl
19	898	99.7	175	9	US-09-754-532-69	Sequence 69, Appl
20	898	99.7	175	9	US-09-754-532-70	Sequence 70, Appl
21	898	99.7	175	9	US-09-754-532-76	Sequence 76, Appl
22	898	99.7	175	9	US-09-754-532-92	Sequence 92, Appl
23	898	99.7	175	9	US-09-754-532-93	Sequence 93, Appl
24	898	99.7	175	9	US-09-754-532-99	Sequence 99, Appl
25	898	99.7	175	9	US-09-818-430A-2	Sequence 2, Appl
26	898	99.7	175	14	US-10-032-108-67	Sequence 67, Appl
27	898	99.7	175	14	US-10-032-108-68	Sequence 68, Appl
28	898	99.7	175	14	US-10-032-108-69	Sequence 69, Appl
29	898	99.7	175	14	US-10-032-108-70	Sequence 70, Appl
30	898	99.7	175	14	US-10-032-108-76	Sequence 76, Appl
31	898	99.7	175	14	US-10-032-108-92	Sequence 92, Appl
32	898	99.7	175	14	US-10-032-108-93	Sequence 93, Appl
33	898	99.7	175	14	US-10-032-108-99	Sequence 99, Appl
34	898	99.7	177	9	US-09-984-186-14	Sequence 14, Appl
35	898	99.7	177	14	US-10-237-667-14	Sequence 14, Appl
36	898	99.7	177	14	US-10-237-708-14	Sequence 14, Appl
37	898	99.7	177	14	US-10-237-866-14	Sequence 14, Appl
38	898	99.7	177	14	US-10-237-871-14	Sequence 14, Appl
39	898	99.7	177	14	US-10-237-824-14	Sequence 14, Appl
40	898	99.7	177	15	US-10-702-536-14	Sequence 14, Appl
41	898	99.7	177	15	US-10-702-636-14	Sequence 14, Appl
42	898	99.7	759	15	US-10-609-346-8	Sequence 8, Appl
43	896	99.4	174	9	US-09-760-008A-1	Sequence 1, Appl
44	896	99.4	174	9	US-09-950-473-2	Sequence 2, Appl
45	896	99.4	174	9	US-09-921-114-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-754-532-2
; Sequence 2, Application US/09754532
; Patent No. US20010016191A1
; GENERAL INFORMATION:
; APPLICANT: Osslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,532
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-754-532-2

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Best Local Similarity 100.0%; Pred. No. 9.3e-84;
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RESULT 2
US-09-230-733-1
; Sequence 1, Application US/09230733
; Patent No. US2002028912A1
; GENERAL INFORMATION:
; APPLICANT: Yamasaki, Motoo
; APPLICANT: Suzawa, Tohiyuki
; APPLICANT: Kobayashi, Ken
; APPLICANT: Konishi, No. US20020028912A1oru
; APPLICANT: Akinaga, Shiro
; APPLICANT: Maruyama, Kumiko
; TITLE OF INVENTION: CHEMICALLY MODIFIED POLYPEPTIDES
; FILE REFERENCE: 249-102
; CURRENT APPLICATION NUMBER: US/09/230,733
; CURRENT FILING DATE: 1998-02-03
; EARLIER APPLICATION NUMBER: PCT/JP98/02504
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: JP 9-149342
; EARLIER FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: polypeptide
; OTHER INFORMATION: having NG-CSF activity
US-09-230-733-1

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RESULT 3
US-09-921-114-2
; Sequence 2, Application US/09921114
; Patent No. US20020177688A1

; GENERAL INFORMATION:
; APPLICANT: ISHIKAWA ET AL
; TITLE OF INVENTION: CHEMICALLY-MODIFIED G-CSF
; FILE REFERENCE: 11009/36193A
; CURRENT APPLICATION NUMBER: US/09/921,114
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 09/518,896
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 08/957,719
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: US 07/983,620
; PRIOR FILING DATE: 1992-11-30
; NUMBER OF SEQ ID NOS: 2
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US-09-921-114-2

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RESULT 4
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; Sequence 2, Application US/09817725
; Publication No. US20040181035A1
; GENERAL INFORMATION:
; APPLICANT: Kinstler, Olaf B.
; APPLICANT: Gabriel, Nancy E.
; APPLICANT: Farrar, Christine B.
; APPLICANT: DePrince, Randolph B.
; TITLE OF INVENTION: N-Terminally Chemically Modified Protein
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Behavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/817,725
; FILING DATE: 26-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/321,510
; FILING DATE: 1994-10-24
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol M.
; REFERENCE/DOCKET NUMBER: A-286
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 175 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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; Publication No. US2003053982A1
; GENERAL INFORMATION:
; APPLICANT: Kinntler, Olaf B.
; Gabriel, Nancy E.
; Farrar, Christine E.
; DePrince, Randolph B.
; TITLE OF INVENTION: N-Terminally Chemically Modified Protein
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
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; FILING DATE: 25-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/321,510
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol M.
; REFERENCE/DOCKET NUMBER: A-286
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-131-956-2

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RESULT 6
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; Sequence 2, Application US/10264846
; Publication No. US20030096400A1
; GENERAL INFORMATION:
; APPLICANT: Kinntler, Olaf B.
; Gabriel, Nancy E.
; Farrar, Christine E.
; DePrince, Randolph B.
; TITLE OF INVENTION: N-Terminally Chemically Modified Protein
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/10/264,846
; FILING DATE: 04-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/321,510
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol M.
; REFERENCE/DOCKET NUMBER: A-286
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-264-846-2

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Best Local Similarity 100.0%; Pred. No. 9.3e-84;
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Db 61 PLSSCPQALQAGLSQLHSGFLYQGLLQALEGISPELGPDLTDLQDLDVADPATTIQQ 120
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Db 121 QMEELGMAPALOPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
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; Sequence 21, Application US/10009792A
; Publication No. US20030153049A1
; GENERAL INFORMATION:
; APPLICANT: LEE, Sang-Yup
; TITLE OF INVENTION: ESCHERICHIA COLI STRAIN SECRETING HUMAN
; FILE REFERENCE: GRANULOCYTE COLONY STIMULATING FACTOR (G-CSF)
; CURRENT APPLICATION NUMBER: US/10/009,792A
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: PCT/KR01/00549
; PRIOR FILING DATE: 2001-03-31
; PRIOR APPLICATION NUMBER: KR 10-2000-0017052
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-009-792A-21

Query Match
Best Local Similarity 100.0%; Score 901; DB 14; Length 175;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MTPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIPWA 60
QY 61 PLSSCPQALQALACLSQLHSGFLYQGLLQALEGISPELGTDLTLDLVADFAATTIQ 120
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QY 121 QMEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 175
DB 121 QMEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 175

RESULT 9
US-10-345-639A-2
; Sequence 2, Application US/10345639A
; Publication No. US20030185795A1
; GENERAL INFORMATION:
; APPLICANT: Habberfield, Alan D.
; TITLE OF INVENTION: Oral Delivery of Chemically Modified Proteins
; FILE REFERENCE: A-285G
; CURRENT APPLICATION NUMBER: US/10/345,639A
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 09/818,430
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 08/910,814
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 08/753,901
; PRIOR FILING DATE: 1996-12-03
; PRIOR APPLICATION NUMBER: 08/379,121
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/361,016
; PRIOR FILING DATE: 1994-12-21
; PRIOR APPLICATION NUMBER: 08/194,187
; PRIOR FILING DATE: 1994-02-08
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-345-639A-2

Query Match
Best Local Similarity 100.0%; Score 901; DB 14; Length 175;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIPWA 60
DB 1 MTPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSIGIPWA 60
QY 61 PLSSCPQALQALACLSQLHSGFLYQGLLQALEGISPELGTDLTLDLVADFAATTIQ 120
DB 61 PLSSCPQALQALACLSQLHSGFLYQGLLQALEGISPELGTDLTLDLVADFAATTIQ 120
QY 121 QMEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 175
DB 121 QMEELGNAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSVYRVLRLHAQP 175

RESULT 10
US-10-365-418-1
; Sequence 1, Application US/10365418
; Publication No. US20030195339A1
; GENERAL INFORMATION:
; APPLICANT: Yamasaki, Motoo
; APPLICANT: Suzuki, Toshiyuki
; APPLICANT: Kobayashi, Ken
; APPLICANT: Konishi, No. US20030195339A1orU
; APPLICANT: Akinaga, Shiro
```

APPLICANT: Maruyama, Kumiko
; TITLE OF INVENTION: CHEMICALLY MODIFIED POLYPEPTIDES
; FILE REFERENCE: 249-102
; CURRENT APPLICATION NUMBER: US/10/365,418
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/230,733
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: PCT/JP98/02504
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: JP 9-149342
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: polypeptide
; OTHER INFORMATION: having hg-CSF activity
US-10-365-418-1

Query Match 100.0%; Score 901; DB 14; Length 175;
Best Local Similarity 100.0%; Pred. No. 9.3e-84;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPGPASSLPSQSLKLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWA 60
DB 1 MTPGPASSLPSQSLKLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWA 60

QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDQDVADPATTIWQ 120
DB 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDQDVADPATTIWQ 120

QY 121 QMEELGMALPQTOGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGMALPQTOGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 11
US-10-436-784-2
; Sequence 2, Application US/10436784
; Publication No. US20030204057A1
; GENERAL INFORMATION:
; APPLICANT: ISHIKAWA ET AL
; TITLE OF INVENTION: CHEMICALLY-MODIFIED G-CSF
; FILE REFERENCE: 11009/36193A
; CURRENT APPLICATION NUMBER: US/10/436,784
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: US 09/518,896
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 08/957,719
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: US 07/983,620
; PRIOR FILING DATE: 1992-11-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-436-784-2

Query Match 100.0%; Score 901; DB 14; Length 175;
Best Local Similarity 100.0%; Pred. No. 9.3e-84;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPGPASSLPSQSLKLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWA 60
DB 1 MTPGPASSLPSQSLKLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWA 60

QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDQDVADPATTIWQ 120

DB 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDQDVADPATTIWQ 120
QY 121 QMEELGMALPQTOGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGMALPQTOGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 12
US-10-168-956A-3
; Sequence 3, Application US/10168956A
; Publication No. US20030219404A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD
; TITLE OF INVENTION: No. US20030219404A1 branched polyalkylene glycol derivatives
; FILE REFERENCE: 766.61
; CURRENT APPLICATION NUMBER: US/10/168,956A
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: JP 99/366312
; PRIOR FILING DATE: 1999-12-24
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Hominidae
US-10-168-956A-3

Query Match 100.0%; Score 901; DB 14; Length 175;
Best Local Similarity 100.0%; Pred. No. 9.3e-84;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPGPASSLPSQSLKLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWA 60
DB 1 MTPGPASSLPSQSLKLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWA 60

QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDQDVADPATTIWQ 120
DB 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDQDVADPATTIWQ 120

QY 121 QMEELGMALPQTOGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGMALPQTOGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 13
US-10-632-695-15
; Sequence 15, Application US/10632695
; Publication No. US20040096945A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peizhi
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEIN VARIANTS OF HG-CSF WITH GRANULOPOIETIC
; FILE REFERENCE: A-67614-3/RMS/RMK
; CURRENT APPLICATION NUMBER: US/10/632,695
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/115,131
; PRIOR FILING DATE: 1999-01-06
; PRIOR APPLICATION NUMBER: US 60/118,831
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 09/479,313
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (2)..()
US-10-632-695-15

Query Match 100.0%; Score 901; DB 15; Length 175;
Best Local Similarity 100.0%; Pred. No. 9.3e-84;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPGLPASSLPQSFLKLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWA 60
DB 1 MTPGLPASSLPQSFLKLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWA 60

QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDQDVADFTTIWQ 120
DB 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDQDVADFTTIWQ 120

QY 121 QMEELGMAPALOPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYRHLHAQP 175
DB 121 QMEELGMAPALOPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYRHLHAQP 175

RESULT 14
US-10-659-295-38
; Sequence 38, Application US/10659295
; Publication No. US20040141946A1
; GENERAL INFORMATION:
; APPLICANT: SCHNEIDER, ARMIN
; APPLICANT: SCHAEBITZ, WOLF-RUEDIGER
; APPLICANT: KOLLMAR, RAINER
; APPLICANT: SCHWAB, STEFAN
; TITLE OF INVENTION: METHODS OF TREATING NEUROLOGICAL CONDITIONS WITH HEMATOPOIETIC OR
; FILE REFERENCE: 229530US
; CURRENT APPLICATION NUMBER: US/10/659,295
; CURRENT FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US/10/331,755
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-659-295-38

Query Match 100.0%; Score 901; DB 16; Length 175;
Best Local Similarity 100.0%; Pred. No. 9.3e-84;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPGLPASSLPQSFLKLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWA 60
DB 1 MTPGLPASSLPQSFLKLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWA 60

QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDQDVADFTTIWQ 120
DB 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDQDVADFTTIWQ 120

QY 121 QMEELGMAPALOPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYRHLHAQP 175
DB 121 QMEELGMAPALOPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYRHLHAQP 175

RESULT 15
US-10-750-797-2
; Sequence 2, Application US/10750797
; Publication No. US20040158041A1
; GENERAL INFORMATION:
; APPLICANT: ISHIKAWA ET AL
; TITLE OF INVENTION: CHEMICALLY-MODIFIED G-CSF
; FILE REFERENCE: 11009/36193A
; CURRENT APPLICATION NUMBER: US/10/750,797
; CURRENT FILING DATE: 2004-01-02
; PRIOR APPLICATION NUMBER: US 09/518,896
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 08/957,719
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: US 07/983,620

; PRIOR FILING DATE: 1992-11-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-750-797-2

Query Match 100.0%; Score 901; DB 16; Length 175;
Best Local Similarity 100.0%; Pred. No. 9.3e-84;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPGLPASSLPQSFLKLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWA 60
DB 1 MTPGLPASSLPQSFLKLEQVRKIQDGAALQEKLCATYKLCHEPELVLLGHSLGIPWA 60

QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDQDVADFTTIWQ 120
DB 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGTDLTLDQDVADFTTIWQ 120

QY 121 QMEELGMAPALOPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYRHLHAQP 175
DB 121 QMEELGMAPALOPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYRHLHAQP 175

Search completed: December 27, 2004, 13:34:27
Job time : 299.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 27, 2004, 13:11:24 ; Search time 63.5 Seconds
(without alignments)
988.624 Million cell updates/sec

Title: 10032108-2

Perfect score: 901

Sequence: 1 MTPPLGPASSLPQSLFKLCLE.....SHLQSFLEVSRYVLRHLAQP 175

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	901	100.0	175	1 AAP71030	Aap71030 Sequence
2	901	100.0	175	1 AAP70732	Aap70732 Sequence
3	901	100.0	175	1 AAP90107	Aap90107 Human gra
4	901	100.0	175	1 AAP90170	Aap90170 Human gra
5	901	100.0	175	1 AAP91070	Aap91070 Human gra
6	901	100.0	175	2 AA08486	Platelet
7	901	100.0	175	2 AA07533	Recombina
8	901	100.0	175	2 AA04394	PEGylated
9	901	100.0	175	2 AA084297	Human gra
10	901	100.0	175	3 AA078936	Granulocyte
11	901	100.0	175	3 AA014851	Human gra
12	901	100.0	175	3 AA097017	Mature gr
13	901	100.0	175	3 AA023758	Human gra
14	901	100.0	175	4 AA067563	Amino aci
15	901	100.0	175	4 AA067502	Human hg-
16	901	100.0	175	4 AA012154	Human hg-
17	901	100.0	175	4 AA02109	Human G-C
18	901	100.0	175	4 AA051536	Recombina
19	901	100.0	175	5 AA019311	Branched
20	901	100.0	175	6 AA097386	Recombina
21	901	100.0	175	8 AA043080	Recombina
22	901	100.0	317	2 AA023600	Recombina
23	898	99.7	175	2 AA056562	G-CSF ana
24	898	99.7	175	2 AA056585	G-CSF ana
25	898	99.7	175	2 AA056555	G-CSF ana

26	898	99.7	175	2 AA056578	G-CSF ana
27	898	99.7	175	2 AA056553	G-CSF ana
28	898	99.7	175	2 AA056554	G-CSF ana
29	898	99.7	175	2 AA056579	G-CSF ana
30	898	99.7	175	2 AA056556	G-CSF ana
31	898	99.7	759	8 AD116718	Human etu
32	898	99.7	783	2 AA039473	Prepro-HS
33	898	99.7	783	7 ADF14930	Human alb
34	898	99.7	783	7 ADF16488	Human alb
35	898	99.7	789	4 AA029880	Novel hum
36	898	99.7	951	7 ADF15113	Human alb
37	898	99.7	951	7 ADF15108	Human alb
38	898	99.7	978	4 AA029709	Novel hum
39	898	99.7	988	4 AA033272	Novel hum
40	896	99.4	174	1 AA080965	G-CSF ded
41	896	99.4	174	1 AA090470	G-colony
42	896	99.4	174	2 AA013679	Granulocyte
43	896	99.4	174	2 AA026909	Human G-C
44	896	99.4	174	2 AA034707	Human CSF
45	896	99.4	174	2 AA002204	Human G-C

ALIGNMENTS

RESULT 1
AAP71030
ID AAP71030 standard; protein; 175 AA.
XX
AC AAP71030;
XX
DT 29-MAY-1991 (first entry)
XX
DE Sequence of human granulocyte colony stimulating factor (hGCSF) type II.
XX
KW Myelogenous leukaemia therapy; neutrophil.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 1
FT /note= "optional"
XX
PN EP231819-A.
XX
PD 12-AUG-1987.
XX
PF 21-JAN-1987; 87EP-00100809.
XX
PR 22-JAN-1986; 86JP-00010281.
XX
PR 21-JAN-1987; 87JP-00010038.
XX
PA (CHUS) CHUGAI SEIYAKU KK.
XX
PI Tamura M, Hattori K;
XX
WPI; 1987-222837/32.
XX
PT Agent for treating myelogenous leukaemia - contains human granulocyte colony stimulating factor.
XX
PS Claim 3; Page 7; 7pp; English.
XX
CC hGCSF is the effective ingredient of an agent for the treatment of myelogenous leukaemia. The agent is used for increasing the no. of peripheral mature neutrophils in patients with myelogenous leukaemia and also prolonging life. Doses are 0.1-500, pref. 5-100 meg, 1-7 times/week.
XX
CC Type II hGCSF may be prepd. as in EP 8601138.7
XX
SQ Sequence 175 AA;

Query Match 100.0%; Score 901; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.9e-90;

Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPPLGPASSLPQSFLKLCLEQVRKIQDGAALQOEKLCATYKLCHEPELVLLGHSLGIPWA 60
 DB 1 MTPPLGPASSLPQSFLKLCLEQVRKIQDGAALQOEKLCATYKLCHEPELVLLGHSLGIPWA 60
 QY 61 PLSSCPSQALQAGCLSQLHSGFLFYQGLLQALEGISPELGPPTLDTLQLDVADFATTIQQ 120
 DB 61 PLSSCPSQALQAGCLSQLHSGFLFYQGLLQALEGISPELGPPTLDTLQLDVADFATTIQQ 120
 QY 121 QMEELGWAPALOPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
 DB 121 QMEELGWAPALOPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 2
 AAP70732
 ID AAP70732 standard; protein; 175 AA.
 AC AAP70732;
 XX
 XX
 XX 25-MAR-2003 (revised)
 DT 26-APR-1991 (first entry)
 XX
 XX Sequence encoded by human granulocyte colony stimulating factor (hpg-CSF)
 DE CDNA with an amino terminal methionine.
 XX
 XX Haematopoietic disorders; therapy; aplastic anaemia;
 KW bone marrow transplant; burn wounds; leukaemia.
 XX
 XX Homo sapiens.
 XX
 XX WO8701132-A.
 XX
 XX 26-FEB-1987.
 XX
 XX 22-AUG-1986; 86WO-US001708.
 XX
 XX 23-AUG-1985; 85US-00768954.
 PR 23-AUG-1985; 85US-00768959.
 PR 03-MAR-1986; 86US-00835548.
 XX
 XX (KIRI) KIRIN AMGEN INC.
 PA (KIRI) KIRIN AMGEN INC.
 PA (AMGE-) AMGEN.
 XX
 XX Souza LM;
 PI
 XX
 XX WPI; 1987-064855/09.
 DR N-PSDB; AAN71091.
 XX
 XX Poly-peptide with granulocyte colony stimulating factor activity - obt'd.
 PT by recombinant DNA procedures for treating haematopoietic disorders.
 XX
 XX Example; pp42-43; 79pp; English.
 XX
 XX The examples describe procedures for the designing of probes for hpg- CSF
 CC cDNA and genomic clones, both of which are claimed. Specifically claimed
 CC are DNA sequences coding for (Ala 1)hpg-CSF; (Ser 36,42,64 and 74)hpg-CSF
 CC and the corresp. Met-1 cpds. The novelty is that hpg- CSF is the prod. of
 CC procarcynotic or eucarcynotic expression of an exogenous DNA sequence. The
 CC construction of hpg-CSF vectors is also described in the examples.
 CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to
 CC correct PA field.)
 XX
 XX Sequence 175 AA;
 SQ

Query Match 100.0%; Score 901; DB 1; Length 175;
 Best Local Similarity 100.0%; Pred. No. 1.9e-90;
 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPPLGPASSLPQSFLKLCLEQVRKIQDGAALQOEKLCATYKLCHEPELVLLGHSLGIPWA 60
 DB 1 MTPPLGPASSLPQSFLKLCLEQVRKIQDGAALQOEKLCATYKLCHEPELVLLGHSLGIPWA 60
 QY 61 PLSSCPSQALQAGCLSQLHSGFLFYQGLLQALEGISPELGPPTLDTLQLDVADFATTIQQ 120
 DB 61 PLSSCPSQALQAGCLSQLHSGFLFYQGLLQALEGISPELGPPTLDTLQLDVADFATTIQQ 120
 QY 121 QMEELGWAPALOPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
 DB 121 QMEELGWAPALOPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 4
 AAP90170
 ID AAP90170 standard; protein; 175 AA.

Db 1 MTPPLGPASSLPQSFLKLCLEQVRKIQDGAALQOEKLCATYKLCHEPELVLLGHSLGIPWA 60
 QY 61 PLSSCPSQALQAGCLSQLHSGFLFYQGLLQALEGISPELGPPTLDTLQLDVADFATTIQQ 120
 DB 61 PLSSCPSQALQAGCLSQLHSGFLFYQGLLQALEGISPELGPPTLDTLQLDVADFATTIQQ 120
 QY 121 QMEELGWAPALOPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
 DB 121 QMEELGWAPALOPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 3
 AAP90107
 ID AAP90107 standard; protein; 175 AA.
 AC AAP90107;
 XX
 XX 25-MAR-2003 (revised)
 DT 27-NOV-1989 (first entry)
 XX
 XX Human granulocyte colony stimulating factor.
 DE Human granulocyte colony stimulating factor; restriction sites;
 KW bone marrow precursor cells.
 XX
 XX Homo sapiens.
 XX
 XX GB2213821-A.
 XX
 XX 23-AUG-1989.
 PD
 XX 23-DEC-1987; 87GB-00030055.
 PF
 XX 23-DEC-1987; 87GB-00030055.
 PR
 XX (BRBI-) BRIT BIO-TECHN LTD.
 PA
 XX Edwards RM;
 PI
 XX WPI; 1989-243775/34.
 DR
 XX Synthetic granulocyte colony stimulating factor gene - incorporating
 PT restriction sites for facilitating cassette mutagenesis and expression.
 XX
 XX Disclosure; Fig 3a; 24pp; English.
 XX
 XX G-CSF stimulates proliferation of specific bone marrow precursor cells
 CC and their differentiation into granulocytes. See also AAN90533. (Updated
 CC on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct
 CC PA field.)
 XX
 XX Sequence 175 AA;
 SQ

Query Match 100.0%; Score 901; DB 1; Length 175;
 Best Local Similarity 100.0%; Pred. No. 1.9e-90;
 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTPPLGPASSLPQSFLKLCLEQVRKIQDGAALQOEKLCATYKLCHEPELVLLGHSLGIPWA 60
 DB 1 MTPPLGPASSLPQSFLKLCLEQVRKIQDGAALQOEKLCATYKLCHEPELVLLGHSLGIPWA 60
 QY 61 PLSSCPSQALQAGCLSQLHSGFLFYQGLLQALEGISPELGPPTLDTLQLDVADFATTIQQ 120
 DB 61 PLSSCPSQALQAGCLSQLHSGFLFYQGLLQALEGISPELGPPTLDTLQLDVADFATTIQQ 120
 QY 121 QMEELGWAPALOPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
 DB 121 QMEELGWAPALOPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 4
 AAP90170
 ID AAP90170 standard; protein; 175 AA.

XX AAP901070;
 XX
 DT 25-MAR-2003 (revised)
 DT 27-NOV-1989 (first entry)
 XX
 DE Human granulocyte colony stimulating factor.
 XX
 KW Human granulocyte colony stimulating factor; restriction sites;
 KW bone marrow precursor cells.
 XX
 OS Homo sapiens.
 XX
 PN GB2213821-A.
 XX
 PD 23-AUG-1989.
 XX
 PF 23-DEC-1987; 87GB-00030055.
 XX
 PR 23-DEC-1987; 87GB-00030055.
 XX
 PA (BRBI-) BRIT BIO-TECHN LTD.
 XX
 PI Edwards RM;
 XX
 DR WPI; 1989-243775/34.
 XX
 PT Synthetic granulocyte colony stimulating factor gene - incorporating
 PT restriction sites for facilitating cassette mutagenesis and expression.
 XX
 PS Disclosure; Fig 3a; 24pp; English.
 XX
 CC G-CSF stimulates proliferation of specific bone marrow precursor cells
 CC and their differentiation into granulocytes. See also AAN90533. (Updated
 CC on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 175 AA;
 XX
 Query Match 100.0%; Score 901; DB 1; Length 175;
 Best Local Similarity 100.0%; Pred. No. 1.9e-90;
 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTPLGASSLPQSFLKLCLEQVRKIQGDGAALQEKLCATYKLCHPBELVLLGHSIGIPWA 60
 DB 1 MTPLGASSLPQSFLKLCLEQVRKIQGDGAALQEKLCATYKLCHPBELVLLGHSIGIPWA 60
 QY 61 PLSSCPQALQAGLSQLHSGFLYQGLLQALEGISPELGTDLTLDQDVADFATTIQ 120
 DB 61 PLSSCPQALQAGLSQLHSGFLYQGLLQALEGISPELGTDLTLDQDVADFATTIQ 120
 QY 121 QMEELGMALOPTQAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
 DB 121 QMEELGMALOPTQAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
 RESULT 5
 AAP91070
 ID AAP91070 standard; protein; 175 AA.
 XX
 AC AAP91070;
 XX
 DT 25-MAR-2003 (revised)
 DT 27-NOV-1989 (first entry)
 XX
 DE Human granulocyte colony stimulating factor.
 XX
 KW Human granulocyte colony stimulating factor; restriction sites;
 KW bone marrow precursor cells.
 XX
 OS Homo sapiens.
 XX
 PN GB2213821-A.

PD 23-AUG-1989.
 XX
 PF 23-DEC-1987; 87GB-00030055.
 XX
 PR 23-DEC-1987; 87GB-00030055.
 XX
 PA (BRBI-) BRIT BIO-TECHN LTD.
 XX
 PI Edwards RM;
 XX
 DR WPI; 1989-243775/34.
 XX
 PT Synthetic granulocyte colony stimulating factor gene - incorporating
 PT restriction sites for facilitating cassette mutagenesis and expression.
 XX
 PS Disclosure; Fig 3a; 24pp; English.
 XX
 CC G-CSF stimulates proliferation of specific bone marrow precursor cells
 CC and their differentiation into granulocytes. See also AAN90533. (Updated
 CC on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 175 AA;
 XX
 Query Match 100.0%; Score 901; DB 1; Length 175;
 Best Local Similarity 100.0%; Pred. No. 1.9e-90;
 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTPLGASSLPQSFLKLCLEQVRKIQGDGAALQEKLCATYKLCHPBELVLLGHSIGIPWA 60
 DB 1 MTPLGASSLPQSFLKLCLEQVRKIQGDGAALQEKLCATYKLCHPBELVLLGHSIGIPWA 60
 QY 61 PLSSCPQALQAGLSQLHSGFLYQGLLQALEGISPELGTDLTLDQDVADFATTIQ 120
 DB 61 PLSSCPQALQAGLSQLHSGFLYQGLLQALEGISPELGTDLTLDQDVADFATTIQ 120
 QY 121 QMEELGMALOPTQAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
 DB 121 QMEELGMALOPTQAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
 RESULT 6
 AAN08486
 ID AAN08486 standard; protein; 175 AA.
 XX
 AC AAN08486;
 XX
 DT 03-MAR-1997 (first entry)
 XX
 DE Platelet growth accelerator.
 XX
 KW Platelet growth accelerator; granulocyte colony stimulating factor;
 KW G-CSF; human; therapy; thrombocytopaenia.
 XX
 OS Homo sapiens.
 XX
 PN WO9523165-A1.
 XX
 PD 31-AUG-1995.
 XX
 PF 23-FEB-1995; 95WO-JP000266.
 XX
 PR 23-FEB-1994; 94JP-00025735.
 XX
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 PI Yamasaki M, Okabe M, Suzawa T, Kobayashi K, Maruyama K;
 XX
 DR WPI; 1995-320309/41.
 XX
 PT Platelet growth accelerator contg. modified hG-CSF - for treatment of
 PT thrombo:cytopaenia.
 XX
 PS Claim 2; Page 35-36; 46pp; Japanese.

XX This sequence represents a platelet growth accelerator of the invention.
CC This sequence contains a human granulocyte colony stimulating factor (G-CSF) peptide. The G-CSF peptide contains at least one amino carboxy, mercapto or guanidino group chemically modified. This platelet growth accelerator can be used in the treatment of thrombocytopaenia
XX Sequence 175 AA;
Query Match 100.0%; Score 901; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.9e-90;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTPGLPASSLPQSFLKLCLEQVRKIQGDGAALQEKLCATYKLCHEPELVLLGHSLGIPWA 60
DB 1 MTPGLPASSLPQSFLKLCLEQVRKIQGDGAALQEKLCATYKLCHEPELVLLGHSLGIPWA 60
QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIQQ 120
DB 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIQQ 120
QY 121 QMEELGWAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYRHLAQP 175
DB 121 QMEELGWAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYRHLAQP 175
RESULT 7
ID AAW07533 standard; protein; 175 AA.
AC AAW07533;
XX 07-MAR-1997 (first entry)
XX Recombinant human G-CSF, for use in novel powder.
XX Powder; granulocyte colony stimulating factor; G-CSF; recombinant; human;
XX saccharide; mannitol; lactose; administration; drug;
XX myelopietic function; improvement; nasal membrane.
XX Homo sapiens.
XX JP08198772-A.
XX 06-AUG-1996.
XX 01-MAR-1995; 95JP-00041734.
XX 25-NOV-1994; 94JP-00291765.
XX (KIRI) KIRIN BREWERY KK.
XX WPI; 1996-408328/41.
XX A powdery compen. contg. G-CSF and a saccharide - for nasal
XX administration, is useful for improving myelopietic functions.
XX Example 1; Page 6; 8pp; Japanese.
XX The novel powder of the invention contains granulocyte colony stimulating
XX factor (G-CSF), e.g. the present sequence, and a saccharide, pref.
XX mannitol or lactose. It can be used for the admin. of G-CSF, an important
XX drug for the improving myelopietic function, via the nasal membranes, as
XX the saccharide enables a higher drug absorability to be attained without
XX damaging the nasal membranes
XX Sequence 175 AA;
Query Match 100.0%; Score 901; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.9e-90;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTPGLPASSLPQSFLKLCLEQVRKIQGDGAALQEKLCATYKLCHEPELVLLGHSLGIPWA 60

DB 1 MTPGLPASSLPQSFLKLCLEQVRKIQGDGAALQEKLCATYKLCHEPELVLLGHSLGIPWA 60
QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIQQ 120
DB 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIQQ 120
QY 121 QMEELGWAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYRHLAQP 175
DB 121 QMEELGWAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYRHLAQP 175
RESULT 8
ID AAR94394 standard; protein; 175 AA.
XX AAR94394;
XX 28-NOV-1996 (first entry)
XX PEGylated recombinant human granulocyte colony stimulating factor.
XX Recombinantly produced; human granulocyte colony stimulating factor;
XX rh-G-CSF; polyethylene glycol; PEG; stable; PEGylated G-CSF;
XX haematopoietic disorder; interferon; cell proliferative disorder;
XX viral infection; autoimmune disorder; multiple sclerosis.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Modified-site 1 /note= "PEGylated-Met"
XX WO9611953-A1.
XX 25-APR-1996.
XX 08-FEB-1995; 95WO-US001729.
XX 12-OCT-1994; 94US-00321510.
XX (AMGE-) AMGEN INC.
XX Kinstler OB, Gabriel NE, Farrar CE, Deprince RB;
XX WPI; 1996-221948/22.
XX N-PSDB; AAT14329.
XX N-terminally chemically modified proteins - partic. G-CSF or consensus
XX interferon modified with polymers, esp. polyethylene glycol.
XX Claim 8; Page 47-48; 76pp; English.
XX This sequence encodes recombinantly produced human granulocyte colony
XX stimulating factor (rh-G-CSF). The G-CSF protein may be N-terminally
XX modified by polyethylene glycol in the preparation of the invention. The
XX PEGylation of the G-CSF makes the protein more stable and therefore more
XX suitable for therapeutic uses. The PEGylated G-CSF can be used for
XX treating haematopoietic disorders. A similarly modified interferon can be
XX used for treating cell proliferative disorders, viral infections or
XX autoimmune disorders, such as multiple sclerosis
XX Sequence 175 AA;
Query Match 100.0%; Score 901; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.9e-90;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTPGLPASSLPQSFLKLCLEQVRKIQGDGAALQEKLCATYKLCHEPELVLLGHSLGIPWA 60
DB 1 MTPGLPASSLPQSFLKLCLEQVRKIQGDGAALQEKLCATYKLCHEPELVLLGHSLGIPWA 60
QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADPATTIQQ 120

Db 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELGPDLTLDVADFAATTWQ 120
QY 121 QMEELGNAPALQPTQGMPPAFASAFORRAGGVVASHLQSFLEVSRYVLRHLAQP 175
Db 121 QMEELGNAPALQPTQGMPPAFASAFORRAGGVVASHLQSFLEVSRYVLRHLAQP 175
RESULT 9
AAW84297
ID AAW84297 standard; protein; 175 AA.
XX AAW84297;
AC AAW84297;
DT 19-MAR-1999 (first entry)
XX Human granulocyte colony stimulating factor (hGCSF).
DE Human granulocyte colony stimulating factor (hGCSF).
XX Human granulocyte colony stimulating factor; hGCSF;
KW chemical modification; hydroxyl group; polyethyleneglycol;
KW platelet reduction; granulocyte reduction.
XX
OS Homo sapiens.
XX
XX WO9855500-A1.
PN 10-DEC-1998.
XX
XX 05-JUN-1998; 98WO-JP002504.
PF 06-JUN-1997; 97JP-00149342.
XX
XX (KYOW) KYOWA HAKKO KOGYO KK.
PA Yamaaki M, Suzawa T, Kobayashi K, Konishi N, Akinaga S;
PI Maruyama K;
XX
XX WPI; 1999-059899/05.
DR New Chemically modified polypeptides especially granulocyte-colony
PT stimulating factor - has hydroxy group modified with polyethylene glycol.
XX
XX Claim 4; Page 34-35; 45pp; Japanese.
PS The present sequence represents human granulocyte colony stimulating
XX factor (hGCSF). The protein was modified to exemplify the invention. The
CC specification describes a method for chemically modifying polypeptides so
CC that at least one of their hydroxyl groups is modified with
CC polyethyleneglycol. The chemically modified proteins are especially
CC useful for preventing a reduction in platelets or granulocytes, and are
CC more active and longer lasting than the unmodified peptides
XX
XX Sequence 175 AA;
QY Query Match 100.0%; Score 901; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.9e-90;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTPPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGHSLGIPWA 60
Db 1 MTPPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGHSLGIPWA 60
QY 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELGPDLTLDVADFAATTWQ 120
Db 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELGPDLTLDVADFAATTWQ 120
QY 121 QMEELGNAPALQPTQGMPPAFASAFORRAGGVVASHLQSFLEVSRYVLRHLAQP 175
Db 121 QMEELGNAPALQPTQGMPPAFASAFORRAGGVVASHLQSFLEVSRYVLRHLAQP 175
RESULT 10
AAW78936
ID AAW78936 standard; protein; 175 AA.
XX AAW78936;
AC AAW78936;
DT 05-JUN-2000 (first entry)
XX Granulocyte colony-stimulation factor (G-CSF) peptide sequence #1.
DE Granulocyte colony-stimulation factor; G-CSF; powder preparation;
KW polymeric drug administration; mucus membrane.
XX
XX Homo sapiens.
XX WO200002574-A1.
PN 20-JAN-2000.
XX
XX 01-JUL-1999; 99WO-JP003563.
PF 08-JUL-1998; 98JP-00192722.
XX 25-MAR-1999; 99JP-00081549.
PR (KIRI) KIRIN AMGEN INC.
PA Nomura H, Ueki Y;
XX
XX WPI; 2000-182173/16.
DR Powder preparation for mucosal administration of polymeric drug, e.g.
PT peptide, protein, antibody, vaccine or antigen.
XX
XX Disclosure; Page 38-39; 45pp; Japanese.
PS This sequence represents a human granulocyte colony-stimulating factor (G
XX -CSF) polypeptide. G-CSF is used in a powder preparation which is
CC administered via the mucus membrane. The preparation comprises a
CC polymeric medicine and a cationic polymer. The preparation is used for
CC the mucosal administration of polymeric pharmaceuticals and has good
CC absorption through the mucous membrane and improved bioavailability
XX
XX Sequence 175 AA;
QY Query Match 100.0%; Score 901; DB 3; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.9e-90;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTPPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGHSLGIPWA 60
Db 1 MTPPLGPASSLPQSFLKLCLEQVRKIQDGAALQEKLCATYKLCHPPELVLLGHSLGIPWA 60
QY 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELGPDLTLDVADFAATTWQ 120
Db 61 PLSSCPQALQAGCLSQLHSGFLYQGLLQALEGISPELGPDLTLDVADFAATTWQ 120
QY 121 QMEELGNAPALQPTQGMPPAFASAFORRAGGVVASHLQSFLEVSRYVLRHLAQP 175
Db 121 QMEELGNAPALQPTQGMPPAFASAFORRAGGVVASHLQSFLEVSRYVLRHLAQP 175
RESULT 11
AAW14851
ID AAW14851 standard; protein; 175 AA.
XX AAW14851;
AC AAW14851;
XX 19-DEC-2000 (first entry)
DT Human granulocyte colony stimulating factor #2.
XX Human granulocyte colony stimulating factor; G-CSF; neutropaenia;
KW bone marrow suppression; infection.
XX
XX Homo sapiens.

XX WO200040728-A1.
 XX 13-JUL-2000.
 XX 06-JAN-2000; 2000WO-US000300.
 XX 06-JAN-1999; 99US-0115131P.
 XX 05-FEB-1999; 99US-0118831P.
 XX (XENC-) XENCOR INC.
 XX Dahiyat B, Luo P;
 XX WPI; 2000-465988/40.
 XX
 XX A non-naturally occurring granulopoietic activity protein (GPA) for
 XX treating granulocyte colony stimulating factor (G-CSF)-responsive disease
 XX comprises an amino acid sequence less than 95% identical to hG-CSF.
 XX
 XX Disclosure; Fig 3; 63pp; English.
 XX
 XX The present sequence is the protein sequence for the human granulocyte
 XX colony stimulating factor (G-CSF). This protein is involved in the
 XX proliferation and differentiation of granulocytes in the blood. The
 XX sequence was used to create the proteins of the invention, which are
 XX designated granulopoietic activity (GPA) proteins. These can be used
 XX instead of G-CSF, which has a short half-life in the blood and is
 XX unstable in storage, in treatments for neutropenia associated with
 XX cancer therapies, radiation accidents, bone marrow transplantation, bone
 XX marrow suppression conditions such as AIDS, myelodysplastic syndromes
 XX characterised by granulocyte functional abnormalities, and severe
 XX infections. They can also be used to enhance peripheral blood progenitor
 XX cell collection
 XX
 XX SQ Sequence 175 AA;

Query Match 100.0%; Score 901; DB 3; Length 175;
 Best Local Similarity 100.0%; Pred. No. 1.9e-90;
 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTPLGPAASSLPQSFLKLCLEQVRKIQDGAALQKLCATYKLCHEPELVLLGHSIGIPWA 60
 DB 1 MTPLGPAASSLPQSFLKLCLEQVRKIQDGAALQKLCATYKLCHEPELVLLGHSIGIPWA 60
 QY 61 PLSSCPQALQALGCLSQLHSGFLYQGLLQALGEGISPELGTDLTLDLQDVADFATTIQ 120
 DB 61 PLSSCPQALQALGCLSQLHSGFLYQGLLQALGEGISPELGTDLTLDLQDVADFATTIQ 120
 QY 121 QMEELGNAPALOPTQGNMPAFASAFQRRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
 DB 121 QMEELGNAPALOPTQGNMPAFASAFQRRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 12
 AAY97017
 ID AAY97017 standard; protein; 175 AA.
 XX AAY97017;
 XX AC
 XX 31-OCT-2000 (first entry)
 XX Mature granulocyte colony stimulating factor.
 XX G-CSF; granulocyte colony stimulating factor; sustained-release;
 XX biocompatible polyol/oil suspension; anti-inflammatory.
 XX Homo sapiens.
 XX WO200038652-A1.
 XX 06-JUL-2000.
 XX

PF 20-DEC-1999; 99WO-US030527.
 XX
 XX 23-DEC-1998; 98US-00221181.
 PR 23-NOV-1999; 99US-00448205.
 XX (AMGE-) AMGEN INC.
 XX Goldenberg MS, Shan D, Beekman AC;
 XX WPI; 2000-452289/39.
 XX
 XX Pharmaceutical composition for the sustained-release of a biologically
 XX active agent (BAA), such as granulocyte-colony stimulating factor,
 XX comprises incorporating the BAA into a biocompatible polyol/oil
 XX suspension.
 XX
 XX Claim 7; Page; 38pp; English.
 XX
 XX A pharmaceutical composition comprising a biologically active agent (BAA)
 XX incorporated into a biocompatible polyol/oil suspension which contains a
 XX thickener is new. The compositions are used for the sustained-release of
 XX a BAA such as an interferon consensus, EPO, granulocyte-colony
 XX stimulating factor, stem cell factor, leptin, tumor necrosis factor-
 XX binding protein, interleukin-1 receptor antagonist, brain derived
 XX neurotrophic factor, glial derived neurotrophic factor, neutrophil factor
 XX 3, osteoprotegerin, granulocyte macrophage colony stimulating factor,
 XX megakaryocyte derived growth factor, keratinocyte growth factor,
 XX thrombopoietin, or novel erythropoiesis stimulating protein (claimed).
 XX The release of a medicament can be controlled to provide longer periods
 XX of consistent release that previous methods of treatment do not achieve,
 XX such as repeated injections. Blood levels of the active ingredient can be
 XX controlled, providing an enhanced prophylactic, therapeutic, or
 XX diagnostic effect as well as greater safety, patient convenience and
 XX patient compliance. The compositions can lead to dose sparing and a lower
 XX cost of protein production. Bioavailability and protein protection,
 XX stability and potency are increased. Note: This sequence is not given in
 XX the specification, it was created using the mature protein starting at
 XX threonine (shown in AAY97017) is given on page 11
 XX
 XX SQ Sequence 175 AA;

Query Match 100.0%; Score 901; DB 3; Length 175;
 Best Local Similarity 100.0%; Pred. No. 1.9e-90;
 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTPLGPAASSLPQSFLKLCLEQVRKIQDGAALQKLCATYKLCHEPELVLLGHSIGIPWA 60
 DB 1 MTPLGPAASSLPQSFLKLCLEQVRKIQDGAALQKLCATYKLCHEPELVLLGHSIGIPWA 60
 QY 61 PLSSCPQALQALGCLSQLHSGFLYQGLLQALGEGISPELGTDLTLDLQDVADFATTIQ 120
 DB 61 PLSSCPQALQALGCLSQLHSGFLYQGLLQALGEGISPELGTDLTLDLQDVADFATTIQ 120
 QY 121 QMEELGNAPALOPTQGNMPAFASAFQRRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
 DB 121 QMEELGNAPALOPTQGNMPAFASAFQRRAGGVLVASHLQSFLEVSRYVLRHLAQP 175

RESULT 13
 AAB23758
 ID AAB23758 standard; protein; 175 AA.
 XX AAB23758;
 XX AC
 XX 10-JAN-2001 (first entry)
 XX Human granulocyte colony stimulating factor protein SEQ ID NO:1.
 XX Granulocyte colony stimulating factor; G-CSF; CRH-G-CSF-R;
 XX protein co-ordinate data; immunostimulant; identification; mutant;
 XX agonist; antagonist; computer modelling; neutropenia;
 XX three dimensional structure; chemotherapy; radiotherapy; cancer.
 XX

OS Homo sapiens.
PN WO200052057-A1.
XX
PD 08-SEP-2000.
XX
PF 02-MAR-2000; 2000WO-JP001217.
XX
PR 04-MAR-1999; 99JP-00056905.
PR 02-AUG-1999; 99JP-00218691.
XX
PA (BIOM-) BIOMOLECULAR ENG RES INST.
XX
PI Aritomi M, Kunishima N, Morikawa K;
XX
DR WPI; 2000-572177/53.
XX
XX Crystals of a complex of granulocyte-colony stimulating factor (G-CSF)
PT with the binding moiety of G-CSF receptor and their crystal structure for
PT design of G-CSF agonists and antagonists for drug use.
XX
XX Claim 3; Page 389-390; 397pp; Japanese.
XX
XX The present invention describes crystals of a protein complex of
CC granulocyte colony stimulating factor (G-CSF) with the binding moiety of
CC G-CSF receptor, which have immunostimulant activity. The three-
CC dimensional structure of the complex obtained from the crystallographic
CC data is used for searching for, identifying, designing and evaluating G-
CC CSF mutants which are agonists or antagonists of the natural G-CSF, by
CC computer modelling or other methods. These are used for the treatment of
CC neutropaenia caused by chemotherapy and radiotherapy of cancer. The
CC present sequence represents the human G-CSF protein, which is used in the
CC exemplification of the present invention
XX
XX Sequence 175 AA;
XX
Query Match 100.0%; Score 901; DB 3; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.9e-90;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTPLGPASSLPQSFLKLCLEQVRKIQGDGAALQEKLCATYKLCHPPELVLLGHSIGPWA 60
DB 1 MTPLGPASSLPQSFLKLCLEQVRKIQGDGAALQEKLCATYKLCHPPELVLLGHSIGPWA 60
QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIQ 120
DB 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIQ 120
QY 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
RESULT 14
ID AAG67563
XX AAG67563 standard; protein; 175 AA.
XX
AC AAG67563;
XX
DT 26-NOV-2001 (first entry)
XX
DE Amino acid sequence of a human polypeptide.
XX
XX Branched polyalkylene glycol; polyalkylene glycol; enzyme; cytokine;
KW hormone; interferon-beta; multiple sclerosis.
XX
XX Homo sapiens.
XX
XX WO200148052-A1.
XX
XX 05-JUL-2001.
XX
XX 22-DEC-2000; 2000WO-JP009159.
XX

XX 24-DEC-1999; 99JP-00366312.
XX
XX (KYOW) KYOWA HAKKO KOGYO KK.
PA
PI Yamaaki M, Suzawa T, Murakami T, Sakurai N, Yamashita K;
PI Mukai M, Kuwabara T, Ohta S, Miki I;
XX
XX WPI; 2001-570380/64.
DR
XX New branched polyalkylene glycols useful for modifying polypeptides such
PT as enzymes, cytokine and hormones.
PT
XX Disclosure; Page 99-100; 103pp; Japanese.
XX
XX The specification describes branched polyalkylene glycols which have two
CC single chain polyalkylene glycols attached to a group having a cyclic
CC structure other than a planar structure and a group reactive with an
CC amino acid side chain, the N-terminal amino group or the C-terminal
CC carboxy group in a polypeptide or a group which can be converted into the
CC reactive group. The branched chain polyalkylene glycols are used for
CC chemically modifying physiologically active polypeptides such as enzymes,
CC cytokines or hormones (preferably interferon-beta for treating multiple
CC sclerosis). The present sequence represents a human polypeptide, which is
CC used in the course of the invention
XX
XX Sequence 175 AA;
XX
Query Match 100.0%; Score 901; DB 4; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.9e-90;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTPLGPASSLPQSFLKLCLEQVRKIQGDGAALQEKLCATYKLCHPPELVLLGHSIGPWA 60
DB 1 MTPLGPASSLPQSFLKLCLEQVRKIQGDGAALQEKLCATYKLCHPPELVLLGHSIGPWA 60
QY 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIQ 120
DB 61 PLSSCPSQALQAGCLSQLHSGFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIQ 120
QY 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
DB 121 QMEELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVSRYVLRHLAQP 175
RESULT 15
ID AAG67502
XX AAG67502 standard; protein; 175 AA.
XX
AC AAG67502;
XX
DT 26-NOV-2001 (first entry)
XX
DE Amino acid sequence of human G-CSF.
XX
XX Leptin; CRH-leptin receptor; weight loss; G-CSF;
KW protein co-ordinate data.
XX
XX Homo sapiens.
XX
XX WO200166593-A1.
XX
XX 13-SEP-2001.
XX
XX 05-MAR-2001; 2001WO-JP001666.
XX
XX 07-MAR-2000; 2000JP-00062404.
XX
XX (BIOM-) BIOMOLECULAR ENG RES INST.
XX
XX Toh H, Hiroike T, Aritomi M, Kunishima N, Morikawa K;
XX
XX WPI; 2001-565574/63.
XX

XX New three-dimensional structural coordinate of a protein complex of
PT leptin and its receptor binding domain, for identifying and designing
PT leptin mutants with superior biological activity, or agonists and
PT antagonists.
XX
PS Example 1; Page 673-674; 683pp; Japanese.
XX
CC The specification describes a three-dimensional (3D) structural
CC coordinate of a complex formed from leptin and a binding domain of its
CC receptor (CRH-leptin receptor). The 3D structural coordinate is
CC applicable in identifying, searching, evaluating or designing leptin
CC mutants with superior biological activity or its agonists and antagonists
CC after mutation or modification, particularly for providing effect on
CC arcuate nuclei, and in inhibiting intake or reducing weight loss. The
CC present sequence represents a human protein, designated G-CSF. The
CC protein is used in the course of the invention
XX
SQ Sequence 175 AA;
Query Match 100.0%; Score 901; DB 4; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.9e-90;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MTPIGPASSLPQSFLKCLQVRIQGDGAALQEKLCATYKLCHELVLLGHSIGIPWA 60
Db 1 MTPIGPASSLPQSFLKCLQVRIQGDGAALQEKLCATYKLCHELVLLGHSIGIPWA 60
Qy 61 PLSSCPQALQALQCLSQLHSGFLYQGLQALEGISPELGPTLDTLQDVADPATTIQ 120
Db 61 PLSSCPQALQALQCLSQLHSGFLYQGLQALEGISPELGPTLDTLQDVADPATTIQ 120
Qy 121 QMEELGNAPALQPTQGAMPAPAFSAFQRRAGGVLVASHLQSFLEVSVYVLRHLAQP 175
Db 121 QMEELGNAPALQPTQGAMPAPAFSAFQRRAGGVLVASHLQSFLEVSVYVLRHLAQP 175

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Job time : 67.5 secs